

OM protein - protein search, using sw model

Run on: January 9, 2004, 12:21:36 ; Search time 39.6051 Seconds  
(without alignments)  
1795.466 Million cell updates/sec

Title: US-09-674-379A-13  
Perfect score: 2533  
Sequence: 1 MPGIKRIITVTILALCLFSP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*  
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*  
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*  
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*  
4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*  
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\*  
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:\*  
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*  
8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:\*  
9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:\*  
10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:\*  
11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:\*  
12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*  
13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:\*  
14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:\*  
15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:\*  
16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:\*  
17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:\*  
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:\*  
19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:\*  
20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*  
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:\*  
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:\*  
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
No.						
1	2533	100.0	448	19	AAW79739	Human EGF protein
2	2533	100.0	448	20	AAW95709	Homo sapiens fetal
3	2533	100.0	448	20	AAW94281	Human extracellular
4	2533	100.0	448	21	AAW57058	Amino acid sequenc
5	2533	100.0	448	21	AAW54989	Full length human
6	2533	100.0	448	22	AAM93573	Human polypeptide,
7	2533	100.0	448	23	AAU75494	Human extracellular
8	2527	99.8	448	20	AAW08063	Human EGF-like hom
9	2527	99.8	448	22	AAU29227	Human PRO polypept
10	2527	99.8	448	22	AAB31183	Amino acid sequenc
11	2527	99.8	448	24	ABU71315	Human PRO210 prote
12	2527	99.8	448	24	ABU72040	Novel human secret
13	2527	99.8	448	24	ABU65772	Human secreted/tra
14	2527	99.8	448	24	ABU66105	Novel human secret
15	2527	99.8	448	24	ABU67141	Novel human secret
16	2527	99.8	448	24	ABU67272	Novel human secret
17	2527	99.8	448	24	ABU67609	Human secreted/tra
18	2527	99.8	448	24	ABU65467	Human PRO polypept
19	2527	99.8	448	24	ABU58603	Human PRO polypept
20	2527	99.8	448	24	ABU56139	Human secreted/tra
21	2527	99.8	448	24	ABU57134	Human PRO polypept
22	2527	99.8	448	24	ABU10713	Human secreted/tra
23	2405	94.9	448	21	AAW56750	Smooth muscle prol
24	2405	94.9	448	21	AAW54990	Full length mouse
25	2376	93.8	461	21	AAW56752	Smooth muscle prol
26	2376	93.8	461	21	AAW54991	Full length mouse
27	2302	90.9	423	21	AAW56751	Smooth muscle prol
28	2302	90.9	423	21	AAW56753	Smooth muscle prol
29	2230	88.0	392	18	AAW31705	Human extracellular
30	1827	72.1	335	21	AAW76008	Rat EGF extracellu
31	1827	72.1	335	22	AAB55947	Skin cell protein,
32	1827	72.1	335	23	ABB72147	Rat protein isolat
33	1289	50.9	443	18	AAW32110	Human extracellular
34	1289	50.9	443	20	AAW16587	Extracellular prot
35	1289	50.9	443	21	AAB33418	Human PRO226 prote
36	1289	50.9	443	21	AAW84707	A human p53 mutant
37	1289	50.9	443	21	AAW55850	Human S1-5 ECMF-li
38	1289	50.9	443	22	AAU12330	Human PRO226 polyp
39	1289	50.9	443	23	AAU86130	Human PRO226 polyp
40	1289	50.9	443	24	ABU66728	Human PRO polypept
41	1289	50.9	443	24	ABU67004	Human secreted/tra
42	1289	50.9	443	24	ABU59809	Novel secreted and
43	1283	50.7	443	22	AAB92533	Human protein sequ
44	1282	50.6	443	21	AAW84706	Amino acid sequenc
45	1237.5	48.9	433	21	AAB58353	Lung cancer associ

# ALIGNMENTS

## RESULT 1

AAW79739

ID AAW79739 standard; Protein; 448 AA.

XX

AC AAW79739;

XX

DT 25-JAN-1999 (first entry)

XX

DE Human EGF protein.

XX

KW Extracellular/epidermal growth factor-like protein; EGF; human; liver;  
KW vascular smooth muscle cell proliferation; neurology; pathology; AIDS;  
KW dementia; ocular; disorder; cornea; inflammation; tumour cell; kidney;  
KW wound; epithelium; surgery; skin graft; ulcer; diabetic; trophic;  
KW Marfan syndrome; treatment; hair follicle; embryogenesis; neoplasma;  
KW epidermal cell; cancer; psoriasis; detection.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..25

FT /label= signal

FT Protein 26..448

FT /label= EGF

FT /note= "Extracellular/epidermal growth factor-like  
FT protein"

FT Region 112..153

FT /label= EGF-1

FT Region 154..190

FT /label= EGF-2

FT Region 191..230

FT /label= EGF-3

FT Region 231..271

FT /label= EGF-4

FT Region 272..314

FT /label= EGF-5

XX

PN W09846746-A1.

XX

PD 22-OCT-1998.

XX

PF 11-APR-1997; 97WO-US06020.

XX

PR 11-APR-1997; 97WO-US06020.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Li H, Olsen HS;

XX

DR WPI; 1998-568728/48.

DR N-PSDB; AAV62432.

XX

PT New isolated extracellular/epidermal growth factor - used for  
PT regulating vascular smooth muscle cell proliferation, e.g. for  
PT enhancing neurological functions or treating neoplasia and other  
PT disorders.

XX

PS Claim 10a; Fig 1A-D; 62pp; English.

XX

CC This sequence represents a novel human extracellular/epidermal growth  
CC factor-like protein, EEGF. This protein can be used to regulate  
CC vascular smooth muscle cell proliferation and for restoration or  
CC enhancement of neurological functions diminished as a result of other  
CC damaging pathologies such as AIDS dementia. The protein can also be used  
CC to treat senile dementia, ocular disorders such as corneal inflammation,  
CC for targeting tumour cells, for treating kidney disorders, for liver  
CC regeneration or treating liver dysfunction, for treating wounds including  
CC all cutaneous wounds, corneal wounds, and injuries to the  
CC epithelial-lined hollow organs of the body or resulting from trauma such  
CC as burns, abrasions and cuts as well as from surgical procedures such as  
CC surgical incisions and skin grafting. The polypeptides can also be used  
CC for treating chronic conditions, such as chronic ulcers, diabetic ulcers,  
CC other non-healing (trophic) conditions, to treat Marfan syndrome, to  
CC promote hair follicular development, to stimulate growth and  
CC differentiation of various epidermal and epithelial cells in vivo and in  
CC vitro and to stimulate embryogenesis. Antagonists to EEGF can be used to  
CC treat neoplasia such as cancers or tumours, skin disorders such as  
CC psoriasis or corneal inflammation. The products can also be used for  
CC identifying EEGF receptors, detection, diagnosis and drug screening.

XX

SQ Sequence 448 AA;

Query Match 100.0%; Score 2533; DB 19; Length 448;  
Best Local Similarity 100.0%; Pred. No. 4e-159;  
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPGIKRILTVTILALCLSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60  
Db 1 MPGIKRILTVTILALCLSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

QY 61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD 120  
Db 61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD 120

QY 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSDTGYWLLLEGQCLDIDECRYGYCQOL 180  
Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSDTGYWLLLEGQCLDIDECRYGYCQOL 180

QY 181 CANVPGSYSTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
Db 181 CANVPGSYSTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

QY 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
Db 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

QY 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPPFTILYRDMDVVSGRS 360  
Db 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPPFTILYRDMDVVSGRS 360

QY 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420  
Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420



QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448  
|||||  
Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 2

AAW95709

ID AAW95709 standard; Protein; 448 AA.

XX

AC AAW95709;

XX

DT 21-JUN-1999 (first entry)

XX

DE Homo sapiens fetal kidney clone AK647 secreted protein.

XX

KW Secreted protein; fetal kidney.

XX

OS Homo sapiens.

XX

PN W09900405-A1.

XX

PD 07-JAN-1999.

XX

PF 29-JUN-1998; 98WO-US13530.

XX

PR 30-JUN-1997; 97US-0885610.

XX

PA (GEMY ) GENETICS INST INC.

XX

PI Agostino MJ, Evans C, Jacobs K, Lavallie ER, Mccoy JM;

PI Merberg D, Racie LA, Treacy M;

XX

DR WPI; 1999-095671/08.

DR N-PSDB; AAX07567.

XX

PT New polynucleotides encoding secreted human proteins - are derived  
PT from foetal kidney or adult retina cDNA libraries, used as, e.g.  
PT potential vaccines

XX

PS Claim 11; Pages 52-54; 76pp; English.

XX

CC The sequence is that of a secreted protein from a human fetal  
CC kidney clone AK296. Such a sequence is predicted to have biological  
CC activities which would make them suitable for treating, preventing or  
CC ameliorating medical conditions in humans and animals, although no  
CC supporting data is given. Suggested activities include nutritional  
CC activity, cytokine and cell proliferation/differentiation activity,  
CC immune stimulating (e.g. as vaccines) or suppressing activity,  
CC haematopoiesis regulating activity, tissue growth activity,  
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
CC activity, cadherin/tumour invasion suppressor activity, and tumour  
CC inhibition activity. It is also stated to be useful for gene  
CC therapy.

XX

SQ Sequence 448 AA;

Query Match 100.0%; Score 2533; DB 20; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 4e-159;  
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1  MPGIKRILVTITLALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
      |||
Db      1  MPGIKRILVTITLALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61  NQNGGYLCIPRTNPVYRGPSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
      |||
Db     61  NQNGGYLCIPRTNPVYRGPSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy    121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLBGQCLDIDECRYGYCQOL 180
      |||
Db    121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLBGQCLDIDECRYGYCQOL 180

Qy    181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
      |||
Db    181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy    241  DGVHCSDMDECSFSEFLCQHECVNQPPTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
      |||
Db    241  DGVHCSDMDECSFSEFLCQHECVNQPPTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

Qy    301  LQQTCTYNLQGGFKCIDPIRCEEPYLRIISDNRCMPAENPGCRDQPFTILYRMDVVSGRS 360
      |||
Db    301  LQQTCTYNLQGGFKCIDPIRCEEPYLRIISDNRCMPAENPGCRDQPFTILYRMDVVSGRS 360

Qy    361  VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPKGPRIQLDL 420
      |||
Db    361  VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPKGPRIQLDL 420

Qy    421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
      |||
Db    421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
  
```

RESULT 3

AAW94281

ID AAW94281 standard; Protein; 448 AA.

XX

AC AAW94281;

XX

DT 07-MAY-1999 (first entry)

XX

DE Human extracellular matrix protein (ECMP)-1.

XX

KW Extracellular matrix protein; ECMP-1; diagnosis; treatment; cancer;

KW immune disorder; human.

XX

OS Homo sapiens.

XX

PN W09900410-A2.

XX

PD 07-JAN-1999.

XX

PF 23-JUN-1998; 98WO-US13012.

XX  
 PR 27-JUN-1997; 97US-0884072.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Bandman O, Corley NC, Guegler KJ;  
 XX  
 DR WPI; 1999-095674/08.  
 DR N-PSDB; AAX05359.  
 XX  
 PT New polynucleotide encoding extracellular matrix protein, ECMP-1 -  
 PT useful in the diagnosis, prevention and treatment of immune  
 PT disorders and cancer  
 XX  
 PS Claim 1; Fig 1A-G; 79pp; English.  
 XX  
 CC This represents a human extracellular matrix protein (ECMP)-1. Host  
 CC cells containing a vector comprising the ECMP-1 nucleic acid are used  
 CC for the recombinant production of the protein. ECMP-1 and its  
 CC (ant)agonists, are useful in the diagnosis, prevention, and treatment  
 CC of cancer and immune disorders.  
 XX  
 SQ Sequence 448 AA;

Query Match 100.0%; Score 2533; DB 20; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 4e-159;  
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPGIKRIILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60  
 |  
 Db 1 MPGIKRIILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60  
 |  
 Qy 61 NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120  
 |  
 Db 61 NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120  
 |  
 Qy 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180  
 |  
 Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180  
 |  
 Qy 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
 |  
 Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
 |  
 Qy 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |  
 Db 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |  
 Qy 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRMDVVSGRS 360  
 |  
 Db 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRMDVVSGRS 360  
 |  
 Qy 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRIKGPRIQLDL 420  
 |  
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRIKGPRIQLDL 420  
 |  
 Qy 421 EMITVNTVINFRGSSVIRLIYVSQYPF 448

Db

421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 4

AAAY57058

ID AAAY57058 standard; Protein; 448 AA.

XX

AC AAAY57058;

XX

DT 21-FEB-2000 (first entry)

XX

DE Amino acid sequence of the human secreted protein AK647.

XX

KW AK647; aortic tissue development; smooth muscle cell modulator; SCID;  
KW nutritional supplement; vasculogenesis; embryonic development; infection;  
KW cytokine activity; cell proliferation; cell differentiation; detect; HIV;  
KW immune deficiency; haematopoiesis regulation; tissue regrowth; diagnose;  
KW wound healing; restenosis; atherosclerosis; drug screen.

XX

OS Homo sapiens.

XX

PN WO9960125-A2.

XX

PD 25-NOV-1999.

XX

PF 18-MAY-1999; 99WO-US10931.

XX

PR 19-MAY-1998; 98US-0081002.

PR 21-MAY-1998; 98US-0083002.

XX

PA (GEMY ) GENETICS INST INC.

XX

PI Jacobs K, McCoy JM, Racie L, LaVallie E, Treacy M, Evans C;  
PI Agostino M, Lu Z, Merberg D;

XX

DR WPI; 2000-053298/04.

DR N-PSDB; AAZ39892.

XX

PT Proteins, and their encoding polynucleotides, used for treating e.g.  
PT smooth muscle cell growth, vasculogenesis, restenosis or  
PT atherosclerosis -

XX

PS Claim 4; Page 46-47; 49pp; English.

XX

CC This is the amino acid sequence of the human secreted protein AK647. The  
CC polynucleotide sequence was obtained from a human foetal kidney cDNA  
CC library. AK647 homologues in chicks and rodents are involved in aortic  
CC tissue development. The spatial and temporal distribution of AK647  
CC indicated that it acts as an a modulator of smooth muscle cells in  
CC vasculogenesis during embryonic development. The primary structure of  
CC AK647 consists of multiple EGF domains. The AK647 protein can be used as  
CC a nutritional source or supplement. The protein shows both inhibitory and  
CC inducing, cytokine, cell proliferation and cell differentiation activity.  
CC The protein may also be used in the treatment of immune deficiencies and  
CC disorders, including severe combined immunodeficiency (SCID), HIV and  
CC other viral, bacterial and fungal infections. Regulation of immune

CC responses may also be carried out by the AK647 protein. Other uses of the  
 CC protein include a role in the regulation of haematopoiesis and in the  
 CC treatment of myeloid and lymphoid cell deficiencies. Uses in bone,  
 CC cartilage, tendon, ligament and nerve tissue regrowth are also possible,  
 CC as well as for wound healing and in the treatment of ulcers and burns.  
 CC The polynucleotides and proteins can be used for preventing, treating or  
 CC ameliorating smooth muscle cell growth, vasculogenesis, restenosis,  
 CC atherosclerosis, blood vessel remodelling and degeneration. The proteins  
 CC may also have activin/inhibin, chemotactic/chemokinetic, haemostatic and  
 CC thrombolytic, receptor/ligand, anti-inflammatory, cadherin/tumour  
 CC invasion suppressor, and tumour inhibition activity. AK647 specific  
 CC antibodies can be used for promoting smooth muscle cell growth or  
 CC vasculogenesis. The proteins and polynucleotides can also be used for  
 CC detection, diagnosis and drug screening.

XX

SQ Sequence 448 AA;

Query Match 100.0%; Score 2533; DB 21; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 4e-159;  
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGCQLDIDECRTIPEACRGDMMCV 60
      |||
Db      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGCQLDIDECRTIPEACRGDMMCV 60

Qy     61  NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYFAAAPPLSAPNYPTISRPLICRFGYQMD 120
      |||
Db     61  NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYFAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy    121  ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQL 180
      |||
Db    121  ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQL 180

Qy    181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCPGYELEE 240
      |||
Db    181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCPGYELEE 240

Qy    241  DGVHCSMDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300
      |||
Db    241  DGVHCSMDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300

Qy    301  LQQTCTYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDPPTILYRMDVVSGRS 360
      |||
Db    301  LQQTCTYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDPPTILYRMDVVSGRS 360

Qy    361  VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTMPIKGPRIQLDL 420
      |||
Db    361  VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTMPIKGPRIQLDL 420

Qy    421  EMITVNTVINFRGSSVIRLRIYSQYFF 448
      |||
Db    421  EMITVNTVINFRGSSVIRLRIYSQYFF 448
  
```

RESULT 5

AAAY54989

ID AAY54989 standard; Protein; 448 AA.

XX  
 AC AAY54989;  
 XX  
 DT 15-FEB-2000 (first entry)  
 XX  
 DE Full length human A55 protein sequence.  
 XX  
 KW A55 protein; human; smooth muscle proliferation; tissue generation;  
 KW vascular smooth muscle cell; arteriosclerosis; tissue reparation; myoma;  
 KW vascular endothelial thickening; haematopoietic cell-regulator; cytokine;  
 KW percutaneous transluminal coronary angioplasty; blood coagulation; PTCA;  
 KW actin; inhibin; chemotaxis; thrombosis; cadherin; therapy;  
 KW tumour metastasis inhibitor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09955864-A1.  
 XX  
 PD 04-NOV-1999.  
 XX  
 PF 28-APR-1999; 99WO-JF02284.  
 XX  
 PR 28-APR-1998; 98JP-0119731.  
 XX  
 PA (ONOH ) ONO PHARM CO LTD.  
 XX  
 PI Honjo T, Tashiro K, Nakamura T;  
 XX  
 DR WPI; 2000-038647/03.  
 DR N-PSDB; AAZ40027.  
 XX  
 PT Novel human polypeptides for treatment of, e.g. arteriosclerosis and  
 PT myoma -  
 XX  
 PS Claim 1; Page 76-80; 87pp; Japanese.  
 XX  
 CC This sequence is the human A55 protein of the invention. The protein  
 CC can be used for the treatment of diseases due to abnormal proliferation  
 CC of smooth muscle. The polypeptides can be used according their inhibition  
 CC of the proliferation of vascular smooth muscle cells, particularly in  
 CC treating arteriosclerosis or re-narrowing by vascular endothelial  
 CC thickening after percutaneous transluminal coronary angioplasty (PTCA),  
 CC or myoma, haematopoietic cell-regulatory activity, cytokine activity,  
 CC tissue generation/reparation activity, actin/inhibin activity, taxis  
 CC and chemotaxis activity, blood coagulation/thrombotic activity,  
 CC receptor/ligand activity, cadherin/tumour metastasis inhibiting activity;  
 CC tumour inhibition, and as a nutrient.  
 XX  
 SQ Sequence 448 AA;

Query Match 100.0%; Score 2533; DB 21; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 4e-159;  
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPGIKRLITVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MPGIKRLITVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy 61 NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120  
 |||  
 Db 61 NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120  
 |||  
 Qy 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQL 180  
 |||  
 Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQL 180  
 |||  
 Qy 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
 |||  
 Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
 |||  
 Qy 241 DGVHCSDMDECSFSEFLCQHECVNPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300  
 |||  
 Db 241 DGVHCSDMDECSFSEFLCQHECVNPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300  
 |||  
 Qy 301 LQQTCCYNLQGGPKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPF TILYRMDVVSGRS 360  
 |||  
 Db 301 LQQTCCYNLQGGPKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPF TILYRMDVVSGRS 360  
 |||  
 Qy 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQDL 420  
 |||  
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQDL 420  
 |||  
 Qy 421 EMITVNTVINFRGSSVIRLRIYVSQYYPF 448  
 |||  
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYYPF 448  
 |||

# RESULT 6

AAM93573

ID AAM93573 standard; Protein; 448 AA.

XX

AC AAM93573;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human polypeptide, SEQ ID NO: 3357.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX

OS Homo sapiens.

XX

PN EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000; 2000EP-0114089.

XX

PR 08-JUL-1999; 99JP-0194486.

PR 11-JAN-2000; 2000JP-0118774.

PR 02-MAY-2000; 2000JP-0183765.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX  
DR WPI; 2001-524255/58.  
DR N-PSDB; AAK94505.

XX  
PT 830 Primers useful for synthesizing full length cDNA clones and their  
PT use in genetic manipulation -  
XX

PS Claim 8; SEQ ID NO 3357; 1380pp + sequence listing; English.  
XX

CC The invention relates to primers for synthesising full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been  
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
CC molecules have been determined. Primers for synthesising the full length  
CC cDNA are useful for clarifying the function of the protein encoded by  
CC the cDNA. The full length clones were obtained by construction of full  
CC length enriched cDNA libraries that were synthesised by the oligo-capping  
CC method. The primers enable the production of the full length cDNA easily  
CC without any special methods. The present sequence is a polypeptide  
CC encoded by a full length human cDNA of the invention.

CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in CD-ROM format directly from EPO.

XX  
SQ Sequence 448 AA;

Query Match 100.0%; Score 2533; DB 22; Length 448;  
Best Local Similarity 100.0%; Pred. No. 4e-159;  
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSQCLDIDECRTIPEACRGDMMCV 60  
Db 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSQCLDIDECRTIPEACRGDMMCV 60  
Qy 61 NQGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYAAAPPLSAPNYPTISRFLICRFGYQMD 120  
Db 61 NQGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYAAAPPLSAPNYPTISRFLICRFGYQMD 120  
Qy 121 ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCTDGYWLLBQCLDIDECRYGYCQQL 180  
Db 121 ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCTDGYWLLBQCLDIDECRYGYCQQL 180  
Qy 181 CANVPGYSYCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
Db 181 CANVPGYSYCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
Qy 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
Db 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
Qy 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPFITILYRMDVVSGRS 360  
Db 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPFITILYRMDVVSGRS 360  
Qy 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRIKGPRIQLDL 420  
Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRIKGPRIQLDL 420



QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448  
 |||  
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 7

AAU75494

ID AAU75494 standard; Protein; 448 AA.

XX

AC AAU75494;

XX

DT 23-APR-2002 (first entry)

XX

DE Human extracellular protein-like/EGF-like protein, EEGF.

XX

KW Human; extracellular protein-like protein; EGF-like;  
 KW protein; epidermal growth factor; EEGF; ATCC 97285; gene therapy;  
 KW vascular smooth muscle cell proliferation; Marfan syndrome;  
 KW wound healing; neurological trauma; acquired immunodeficiency syndrome;  
 KW AIDS-related dementia; ocular disorder; kidney disorder; liver disorder;  
 KW hair follicle growth promotion; burn; ulcer; corneal incision;  
 KW corneal inflammation; neoplasm; psoriasis.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide

1..25

FT

/label= Signal\_peptide

FT

Protein

26..448

FT

/label= Mature\_EEGF

FT

/note= "This region is specifically claimed in claim 10"

FT

Domain

112..153

FT

/label= EGF\_1\_domain

FT

/note= "This domain is specifically claimed in claim 10"

FT

Domain

154..190

FT

/label= EGF\_2\_domain

FT

/note= "This domain is specifically claimed in claim 10"

FT

Domain

191..230

FT

/label= EGF\_3\_domain

FT

/note= "This domain is specifically claimed in claim 10"

FT

Domain

231..271

FT

/label= EGF\_4\_domain

FT

/note= "This domain is specifically claimed in claim 10"

FT

Domain

272..314

FT

/label= EGF\_5\_domain

FT

/note= "This domain is specifically claimed in claim 10"

XX

PN US2001051358-A1.

XX

PD 13-DEC-2001.

XX

PF 25-MAR-1999; 99US-0275805.

XX

PR 11-APR-1997; 97US-0839525.

PR

10-APR-1996; 96WO-US05247.

XX

PA (OLSE/) OLSEN H S.

Qy	1	MPGIKRILTVTILALCLPSPGMAQAQCTNGFDLDRGSQCLDIDECRTTPEACRGDMMCV	60
Db	1	MPGIKRILTVTILALCLPSPGMAQAQCTNGFDLDRGSQCLDIDECRTTPEACRGDMMCV	60
Qy	61	NQNGGYLCIPRTNPVYRGPSNPYSTPYSGPYAPAAAPLSAPNYPTISRPLICRFGYQMD	120
Db	61	NQNGGYLCIPRTNPVYRGPSNPYSTPYSGPYAPAAAPLSAPNYPTISRPLICRFGYQMD	120
Qy	121	ESNQCVDVDECATDSHCNQPTQICINTEGGYTCSCSDGYWLLGQCLDIDECRYGYCQOL	180
Db	121	ESNQCVDVDECATDSHCNQPTQICINTEGGYTCSCSDGYWLLGQCLDIDECRYGYCQOL	180
Qy	181	CANVPGSYSTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNITYGSFICRCDPGYLEE	240
Db	181	CANVPGSYSTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNITYGSFICRCDPGYLEE	240
Qy	241	DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSPPGYILLDDNRSQDINECEHRNHTCN	300
Db	241	DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSPPGYILLDDNRSQDINECEHRNHTCN	300

QY 301 LQQTTCYNLQGGPKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPPTILYRDMDVVSGRS 360  
 |||  
 Db 301 LQQTTCYNLQGGPKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPPTILYRDMDVVSGRS 360  
 |||  
 QY 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRIKGPRIQLDL 420  
 |||  
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRIKGPRIQLDL 420  
 |||  
 QY 421 EMITVNTVINFRGSSVIRLRIYVSQYFF 448  
 |||  
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYFF 448  
 |||

# RESULT 8

AAAY08063

ID AAY08063 standard; Protein; 448 AA.

XX

AC AAY08063;

XX

DT 11-SEP-2000 (first entry)

XX

DE Human EGF-like homologue protein (PRO217) encoded by DNA32279 cDNA.

XX

KW Inflammatory cell infiltration; immune response; T cell proliferation;  
 KW anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy;  
 KW T cell-mediated disease; spondyloarthropathy; sclerosis; renal disease;  
 KW inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis;  
 KW diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome;  
 KW multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy;  
 KW sclerosing cholangitis; inflammatory bowel disease; Whipple's disease;  
 KW skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor;  
 KW food hypersensitivity; urticaria; eosinophilic pneumonia; transplant;  
 KW idiopathic pulmonary fibrosis; graft rejection; PRO245; human; PRO217;  
 KW EGF-like.

XX

OS Homo sapiens.

XX

FN W09914241-A2.

XX

PD 25-MAR-1999.

XX

PF 17-SEP-1998; 98WO-US19437.

XX

PR 17-SEP-1997; 97US-0059119.

PR 18-SEP-1997; 97US-0059263.

PR 28-OCT-1997; 97US-0063550.

PR 12-NOV-1997; 97US-0065186.

PR 21-NOV-1997; 97US-0066364.

PR 24-NOV-1997; 97US-0066770.

PR 04-JUN-1998; 98US-0088026.

XX

PA (GETH ) GENENTECH INC.

XX

PI Fong S, Goddard A, Gurney AL, Tumas D, Wood WI;

XX

DR WPI; 1999-229499/19.

DR N-PSDB; AAX37670.

XX  
PT Composition containing novel polypeptide PRO245, its agonist or  
PT antagonist -  
XX  
XX  
PS Example 1; Fig 6A; 177pp; English.  
XX  
CC This invention describes a novel composition containing (apart from a  
CC carrier or excipient), a novel PRO245 polypeptide (I), its agonist or  
CC antagonist, or their fragments, for modulating: (i) infiltration of  
CC inflammatory cells into tissue; (ii) an immune response; or (iii) T cell  
CC proliferation. The composition increases or decreases any of the effects  
CC (i)-(iii). The products of the invention have anti-inflammatory,  
CC anti-autoimmune and anti-diabetic activity. (I), and its (ant)agonists  
CC and their fragments, are used to treat immune-related diseases,  
CC particularly T cell-mediated diseases. The diseases treated include  
CC systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic  
CC arthritis, spondyloarthropathies, systemic sclerosis (scleroderma),  
CC idiopathic inflammatory myopathies (dermatomyositis, polymyositis),  
CC Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune  
CC hemolytic anemia (immune pancytopenia, paroxysmal nocturnal  
CC hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic  
CC purpura immune-mediated thrombocytopenia), thyroiditis (Grave's disease,  
CC Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic  
CC thyroiditis), diabetes mellitus, immune-mediated renal disease  
CC (glomerulonephritis, tubulointerstitial nephritis), multiple sclerosis,  
CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic  
CC inflammatory demyelinating polyneuropathy, infectious hepatitis  
CC (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune  
CC chronic active hepatitis, primary biliary cirrhosis, granulomatous  
CC hepatitis, and sclerosing cholangitis, inflammatory bowel disease  
CC (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and  
CC Whipple's disease. Autoimmune or immune-mediated skin diseases including  
CC bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis,  
CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,  
CC urticaria, eosinophilic pneumonia, idiopathic pulmonary fibrosis,  
CC hypersensitivity pneumonitis, and transplantation associated diseases  
CC (graft rejection, and graft-versus-host-disease). (I), its (ant)agonists  
CC or fragment can also be used as an adjuvant in treatment of tumors.  
CC Antibodies against (I) can also be used for diagnosing such diseases.  
CC This sequence represents a human EGF-like homologue encoded by cDNA clone  
CC DNA32279 which is described in the invention.  
XX  
SQ Sequence 448 AA;

Query Match 99.8%; Score 2527; DB 20; Length 448;  
Best Local Similarity 99.8%; Pred. No. 9.9e-159;  
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy      1  MPGIKRLITVTILALCLPSPGNAQAQCTNGFDLRQSQCLDIDECRTIPEACRGDMMCV 60
Db      1  MPGIKRLITVTILALCLPSPGNAQAQCTNGFDLRQSQCLDIDECRTIPEACRGDMMCV 60

Qy      61  NQNGGYLCIPRTNPVYRGPSNPYSTFPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
Db      61  NQNGGYLCIPRTNPVYRGPSNPYSTFPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy      121  ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCTDGYWLLGQCLDIDECRYGYCQQL 180

```

Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLBQCLDIDECRYGYCQQL 180  
 Qy 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
 Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSGLICRCDPGYELEE 240  
 Qy 241 DGVHCSDMDBCSFSEFLQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 Db 241 DGVHCSDMDBCSFSEFLQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 Qy 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPFPTILYRMDVVSGRS 360  
 Db 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPFPTILYRMDVVSGRS 360  
 Qy 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTMPIKGPRIQLDL 420  
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTMPIKGPRIQLDL 420  
 Qy 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448  
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 9

AAU29227

ID AAU29227 standard; Protein; 448 AA.

XX

AC AAU29227;

XX

DT 18-DEC-2001 (first entry)

XX

DE Human PRO polypeptide sequence #204.

XX

KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200168848-A2.

XX

PD 20-SEP-2001.

XX

PF 28-FEB-2001; 2001WO-US06520.

XX

PR 01-MAR-2000; 2000WO-US05601.

PR 02-MAR-2000; 2000WO-US05841.

PR 03-MAR-2000; 2000US-187202P.

PR 06-MAR-2000; 2000US-186968P.

PR 14-MAR-2000; 2000US-189320P.

PR 14-MAR-2000; 2000US-189328P.

PR 15-MAR-2000; 2000WO-US06884.

PR 21-MAR-2000; 2000US-190828P.

PR 21-MAR-2000; 2000US-191007P.

PR 21-MAR-2000; 2000US-191048P.

PR 21-MAR-2000; 2000US-191314P.  
PR 28-MAR-2000; 2000US-192655P.  
PR 29-MAR-2000; 2000US-193032P.  
PR 29-MAR-2000; 2000US-193053P.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 04-APR-2000; 2000US-194449P.  
PR 04-APR-2000; 2000US-194647P.  
PR 11-APR-2000; 2000US-195975P.  
PR 11-APR-2000; 2000US-196000P.  
PR 11-APR-2000; 2000US-196187P.  
PR 11-APR-2000; 2000US-196690P.  
PR 11-APR-2000; 2000US-196820P.  
PR 18-APR-2000; 2000US-198121P.  
PR 18-APR-2000; 2000US-198585P.  
PR 25-APR-2000; 2000US-199397P.  
PR 25-APR-2000; 2000US-199550P.  
PR 25-APR-2000; 2000US-199654P.  
PR 03-MAY-2000; 2000US-201516P.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 05-JUN-2000; 2000US-209832P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 22-AUG-2000; 2000US-0644848.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.

XX

(GETH ) GENENTECH INC.

XX

PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2001-602746/68.

DR

N-PSDB; AAS46128.

XX

PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
PT presence of tumours, such as prostate and breast tumours, in mammals and  
PT to screen for modulators of the compounds -

XX

PS Claim 11; Fig 408; 774pp; English.

XX

CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
CC The PRO polypeptides and their associated nucleic acids can be used to  
CC detect the presence of a tumour in a mammal by comparing the level of  
CC expression of a PRO polypeptide in a test sample of cells from the animal  
CC and a control sample of normal cells, whereby a higher level of  
CC expression in the test sample indicates the presence of a tumour in the  
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
CC and rabbits but are preferably human. The polypeptides can be used to  
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
CC when contacted with it. A specific polypeptide can be used to stimulate  
CC the proliferation or differentiation of chondrocyte cells. The PRO  
CC proteins can be used to determine the presence of tumours and also  
CC susceptibility to tumour development, particularly adrenal, lung, colon,



KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;  
 KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /note= "signal peptide"  
 FT Modified-site 21..27  
 FT /note= "N-myristoylation site"  
 FT Binding-site 54..57  
 FT /note= "cell attachment site"  
 FT Modified-site 64..70  
 FT /note= "N-myristoylation site"  
 FT Modified-site 144..156  
 FT /note= "aspartic acid and asparagine hydroxylation site"  
 FT Modified-site 149..155  
 FT /note= "N-myristoylation site"  
 FT Modified-site 186..192  
 FT /note= "N-myristoylation site"  
 FT Modified-site 226..232  
 FT /note= "N-myristoylation site"  
 FT Modified-site 242..248  
 FT /note= "N-myristoylation site"  
 FT Modified-site 267..273  
 FT /note= "N-myristoylation site"  
 FT Modified-site 283..287  
 FT /note= "N-glycosylation site"  
 FT Modified-site 296..300  
 FT /note= "N-glycosylation site"  
 FT Modified-site 310..316  
 FT /note= "N-myristoylation site"  
 XX  
 PN WO200077037-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 22-MAY-2000; 2000WO-US14042.  
 XX  
 PR 15-JUN-1999; 99US-0139695.  
 PR 20-JUL-1999; 99US-0145070.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 17-AUG-1999; 99US-0149396.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 07-DEC-1999; 99US-0169495.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05841.



PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.

XX

PA

(GETH ) GENENTECH INC.

XX

PI

Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;  
Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;  
Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;  
Wood WI, Zhang Z;

PI

XX

DR

WPI; 2001-050091/06.

DR

N-PSDB; AAC86968.

XX

PT

Isolated nucleic acid molecule encoding a PRO polypeptide which is a  
transmembrane polypeptide is useful for gene therapy and identification  
of related polypeptides -

PT

XX

PS

Claim 12; Fig 10; 244pp; English.

XX

CC

The present sequence represents a human secreted and transmembrane  
polypeptide. The specification describes human polypeptides, designated  
PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,  
PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,  
PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,  
PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,  
PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells  
can be modulated with agents that bind to these polypeptides, resulting  
in the death of the cells. The polynucleotides encoding these  
polypeptides are useful in the recombinant production of the  
polypeptides, as a hybridisation probe to screen libraries to isolate  
homologous sequences, or to map the gene. They may also be used for  
analysing genetic disorders, and to produce transgenic animals which are  
useful for the development and screening of therapeutically useful  
reagents. The polynucleotides can also be used in gene therapy e.g. to  
replace a defective gene.

CC

XX

SQ

Sequence 448 AA;

Query Match 99.8%; Score 2527; DB 22; Length 448;  
Best Local Similarity 99.8%; Pred. No. 9.9e-159;  
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MPGIKRLITVTILALCLPSPGNAQAQCTNGFDLDRQSQCLDIDECRTIPEACRGDMMCV	60
Db	1	MPGIKRLITVTILALCLPSPGNAQAQCTNGFDLDRQSQCLDIDECRTIPEACRGDMMCV	60
Qy	61	NQNGGYLCIPRTNPVYRGPSYSNFYSTPYSGYPAAAPLSAPNYPTISRFLICRFGYQMD	120
Db	61	NQNGGYLCIPRTNPVYRGPSYSNFYSTPYSGYPAAAPLSAPNYPTISRFLICRFGYQMD	120
Qy	121	ESNQCVDVDECATDSHCNPTQICINTEGGYTCSTDGYWLLLEGQCLDIDECRYGYCQQL	180
Db	121	ESNQCVDVDECATDSHCNPTQICINTEGGYTCSTDGYWLLLEGQCLDIDECRYGYCQQL	180

QY 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
 |||||||  
 Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
 |||||||  
 QY 241 DGVHCSDMDECSFSEFLCQHECVNPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |||||||  
 Db 241 DGVHCSDMDECSFSEFLCQHECVNPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |||||||  
 QY 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFPTILYRMDVVSGRS 360  
 |||||||  
 Db 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFPTILYRMDVVSGRS 360  
 |||||||  
 QY 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPKGPRIQLDL 420  
 |||||||  
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPKGPRIQLDL 420  
 |||||||  
 QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448  
 |||||||  
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448  
 |||||||

RESULT 11

ABU71315

ID ABU71315 standard; Protein; 448 AA.

XX

AC ABU71315;

XX

DT 10-JUN-2003 (first entry)

XX

DE Human PRO210 protein.

XX

KW Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood;  
 KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;  
 KW differentiation; tumour; gene therapy.

XX

OS Homo sapiens.

XX

PN US2003036143-A1.

XX

PD 20-FEB-2003.

XX

PF 02-JUL-2002; 2002US-0187600.

XX

PR 16-SEP-1998; 98WO-US19330.

PR 07-OCT-1998; 98WO-US21141.

PR 01-DEC-1998; 98WO-US25108.

PR 08-MAR-1999; 99WO-US05028.

PR 14-MAY-1999; 99WO-US10733.

PR 02-JUN-1999; 99WO-US12252.

PR 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.

PR 01-DEC-1999; 99WO-US28301.

PR 02-DEC-1999; 99WO-US28551.

PR 30-DEC-1999; 99WO-US31274.

PR 05-JAN-2000; 2000WO-US00219.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 29-AUG-2001; 2001WO-US27099.  
PR 18-SEP-1997; 97US-059263P.  
PR 18-SEP-1997; 97US-059266P.  
PR 17-OCT-1997; 97US-062250P.  
PR 21-OCT-1997; 97US-063486P.  
PR 24-OCT-1997; 97US-063120P.  
PR 24-OCT-1997; 97US-063121P.  
PR 28-OCT-1997; 97US-063540P.  
PR 28-OCT-1997; 97US-063541P.  
PR 28-OCT-1997; 97US-063544P.  
PR 28-OCT-1997; 97US-063564P.  
PR 29-OCT-1997; 97US-063734P.  
PR 31-OCT-1997; 97US-063870P.  
PR 31-OCT-1997; 97US-064103P.  
PR 13-NOV-1997; 97US-065311P.  
PR 21-NOV-1997; 97US-066120P.  
PR 24-NOV-1997; 97US-066466P.  
PR 24-NOV-1997; 97US-066772P.  
PR 11-DEC-1997; 97US-069335P.  
PR 12-DEC-1997; 97US-069425P.  
PR 17-DEC-1997; 97US-069870P.  
PR 18-DEC-1997; 97US-068017P.  
PR 10-MAR-1998; 98US-077450P.  
PR 11-MAR-1998; 98US-077632P.  
PR 11-MAR-1998; 98US-077649P.  
PR 20-MAR-1998; 98US-078886P.  
PR 20-MAR-1998; 98US-078939P.  
PR 27-MAR-1998; 98US-079664P.  
PR 27-MAR-1998; 98US-079786P.  
PR 31-MAR-1998; 98US-080107P.  
PR 31-MAR-1998; 98US-080194P.  
PR 01-APR-1998; 98US-080327P.  
PR 01-APR-1998; 98US-080333P.  
PR 08-APR-1998; 98US-081049P.  
PR 08-APR-1998; 98US-081070P.  
PR 09-APR-1998; 98US-081195P.  
PR 15-APR-1998; 98US-081838P.

PR	21-APR-1998;	98US-082568P.
PR	21-APR-1998;	98US-082569P.
PR	22-APR-1998;	98US-082704P.
PR	22-APR-1998;	98US-082797P.
PR	28-APR-1998;	98US-083322P.
PR	29-APR-1998;	98US-083495P.
PR	29-APR-1998;	98US-083496P.
PR	29-APR-1998;	98US-083499P.
PR	29-APR-1998;	98US-083559P.
PR	05-MAY-1998;	98US-084366P.
PR	06-MAY-1998;	98US-084414P.
PR	07-MAY-1998;	98US-084639P.
PR	07-MAY-1998;	98US-084640P.
PR	07-MAY-1998;	98US-084643P.
PR	15-MAY-1998;	98US-085579P.
PR	15-MAY-1998;	98US-085580P.
PR	15-MAY-1998;	98US-085582P.
PR	15-MAY-1998;	98US-085700P.
PR	18-MAY-1998;	98US-086023P.
PR	22-MAY-1998;	98US-086392P.
PR	22-MAY-1998;	98US-086486P.
PR	28-MAY-1998;	98US-087098P.
PR	28-MAY-1998;	98US-087208P.
PR	02-JUN-1998;	98US-087609P.
PR	02-JUN-1998;	98US-087759P.
PR	03-JUN-1998;	98US-087827P.
PR	04-JUN-1998;	98US-088025P.
PR	04-JUN-1998;	98US-088028P.
PR	04-JUN-1998;	98US-088029P.
PR	04-JUN-1998;	98US-088033P.
PR	04-JUN-1998;	98US-088326P.
PR	05-JUN-1998;	98US-088167P.
PR	05-JUN-1998;	98US-088202P.
PR	05-JUN-1998;	98US-088212P.
PR	05-JUN-1998;	98US-088217P.
PR	09-JUN-1998;	98US-088655P.
PR	10-JUN-1998;	98US-088722P.
PR	10-JUN-1998;	98US-088738P.
PR	10-JUN-1998;	98US-088740P.
PR	10-JUN-1998;	98US-088811P.
PR	10-JUN-1998;	98US-088824P.
PR	10-JUN-1998;	98US-088825P.
PR	10-JUN-1998;	98US-088826P.
PR	11-JUN-1998;	98US-088861P.
PR	11-JUN-1998;	98US-088863P.
PR	11-JUN-1998;	98US-088876P.
PR	12-JUN-1998;	98US-089090P.
PR	12-JUN-1998;	98US-089105P.
PR	16-JUN-1998;	98US-089512P.
PR	16-JUN-1998;	98US-089514P.
PR	17-JUN-1998;	98US-089538P.
PR	17-JUN-1998;	98US-089598P.
PR	17-JUN-1998;	98US-089653P.
PR	18-JUN-1998;	98US-089908P.
PR	19-JUN-1998;	98US-089952P.
PR	22-JUN-1998;	98US-090246P.
PR	22-JUN-1998;	98US-090252P.

PR 22-JUN-1998; 98US-090254P.  
 PR 24-JUN-1998; 98US-090429P.  
 PR 24-JUN-1998; 98US-090435P.  
 PR 24-JUN-1998; 98US-090444P.  
 PR 24-JUN-1998; 98US-090461P.  
 PR 24-JUN-1998; 98US-090535P.  
 PR 24-JUN-1998; 98US-090540P.  
 PR 25-JUN-1998; 98US-090676P.  
 PR 25-JUN-1998; 98US-090678P.  
 PR 25-JUN-1998; 98US-090688P.  
 PR 25-JUN-1998; 98US-090690P.  
 PR 25-JUN-1998; 98US-090694P.  
 PR 25-JUN-1998; 98US-090695P.  
 PR 25-JUN-1998; 98US-090696P.  
 PR 26-JUN-1998; 98US-090862P.  
 PR 26-JUN-1998; 98US-090863P.  
 PR 26-JUN-1998; 98US-091010P.  
 PR 01-JUL-1998; 98US-091359P.  
 PR 01-JUL-1998; 98US-091544P.  
 PR 02-JUL-1998; 98US-091478P.  
 PR 02-JUL-1998; 98US-091486P.  
 PR 02-JUL-1998; 98US-091626P.  
 PR 02-JUL-1998; 98US-091628P.  
 PR 02-JUL-1998; 98US-091632P.  
 PR 24-JUL-1998; 98US-094006P.  
 PR 04-AUG-1998; 98US-095282P.  
 PR 10-AUG-1998; 98US-095998P.  
 PR 10-AUG-1998; 98US-096012P.  
 PR 17-AUG-1998; 98US-096757P.  
 PR 17-AUG-1998; 98US-096766P.  
 PR 17-AUG-1998; 98US-096867P.  
 PR 17-AUG-1998; 98US-096891P.  
 PR 17-AUG-1998; 98US-096897P.  
 PR 18-AUG-1998; 98US-096949P.  
 PR 18-AUG-1998; 98US-096959P.  
 PR 18-AUG-1998; 98US-097022P.  
 PR 26-AUG-1998; 98US-097952P.  
 PR 26-AUG-1998; 98US-097954P.  
 PR 26-AUG-1998; 98US-097955P.  
 PR 26-AUG-1998; 98US-097971P.  
 PR 26-AUG-1998; 98US-097974P.  
 PR 26-AUG-1998; 98US-098014P.  
 PR 01-SEP-1998; 98US-098716P.  
 PR 01-SEP-1998; 98US-098723P.  
 PR 02-SEP-1998; 98US-098803P.  
 PR 02-SEP-1998; 98US-098821P.  
 PR 02-SEP-1998; 98US-098843P.  
 PR 09-SEP-1998; 98US-099602P.  
 PR 10-SEP-1998; 98US-099741P.  
 PR 10-SEP-1998; 98US-099754P.  
 PR 10-SEP-1998; 98US-099763P.  
 PR 10-SEP-1998; 98US-099812P.

Query Match 99.8%; Score 2527; DB 24; Length 448;  
 Best Local Similarity 99.8%; Pred. No. 9.9e-159;  
 Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60  
 |||||  
 Db 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60  
 |||||  
 Qy 61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGYPAAAPPLSAPNYPTISRLICRFGYQMD 120  
 |||||  
 Db 61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGYPAAAPPLSAPNYPTISRLICRFGYQMD 120  
 |||||  
 Qy 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLBEGQCLDIDECRYGYCQQL 180  
 |||||  
 Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLBEGQCLDIDECRYGYCQQL 180  
 |||||  
 Qy 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
 |||||  
 Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
 |||||  
 Qy 241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |||||  
 Db 241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |||||  
 Qy 301 LQQTCYNLQGGFKCIDPIRCBEPYLRISDNRCMPAENPGCRDQPFITILYRMDVVSGRS 360  
 |||||  
 Db 301 LQQTCYNLQGGFKCIDPIRCBEPYLRISDNRCMPAENPGCRDQPFITILYRMDVVSGRS 360  
 |||||  
 Qy 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPICKGPREIQLDL 420  
 |||||  
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPICKGPREIQLDL 420  
 |||||  
 Qy 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448  
 |||||  
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448  
 |||||

RESULT 12

ABU72040

ID ABU72040 standard; Protein; 448 AA.

XX

AC ABU72040;

XX

DT 11-JUN-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO210.

XX

KW Human; secreted and transmembrane polypeptide; PRO;  
 KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;  
 KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;  
 KW FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;  
 KW toxin; radiolabel; antibody; cell death; chromosome mapping;  
 KW gene mapping; transgenic animal; knockout animal; gene therapy;  
 KW tissue typing.

XX

OS Homo sapiens.

XX

PN US2002177165-A1.

XX

PD 28-NOV-2002.

XX

PF 01-FEB-2002; 2002US-0066500.  
XX  
PR 14-JUL-1998; 98WO-US14552.  
PR 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19093.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 20-NOV-1998; 98WO-US24855.  
PR 25-NOV-1998; 98WO-US25190.  
PR 01-DEC-1998; 98WO-US25108.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 02-DEC-1999; 99WO-US28565.  
PR 20-DEC-1999; 99WO-US30999.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 09-MAR-2000; 2000WO-US06471.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 26-AUG-1997; 97US-056974P.  
PR 17-SEP-1997; 97US-059115P.  
PR 18-SEP-1997; 97US-059263P.  
PR 19-SEP-1997; 97US-059588P.  
PR 17-OCT-1997; 97US-062285P.  
PR 24-OCT-1997; 97US-062816P.  
PR 24-OCT-1997; 97US-063082P.  
PR 27-OCT-1997; 97US-063329P.  
PR 29-OCT-1997; 97US-063733P.  
PR 21-NOV-1997; 97US-066364P.  
PR 25-NOV-1997; 97US-066840P.  
PR 16-DEC-1997; 97US-069694P.  
PR 09-FEB-1998; 98US-074086P.

PR 09-FEB-1998; 98US-074092P.  
PR 25-MAR-1998; 98US-079294P.  
PR 08-APR-1998; 98US-081049P.  
PR 10-AUG-1998; 98US-095998P.  
PR 18-AUG-1998; 98US-097000P.  
PR 09-SEP-1998; 98US-099601P.  
PR 10-SEP-1998; 98US-099803P.  
PR 10-SEP-1998; 98US-099811P.  
PR 10-SEP-1998; 98US-099812P.  
PR 17-SEP-1998; 98US-100858P.  
PR 24-SEP-1998; 98US-101922P.  
PR 28-OCT-1998; 98US-106032P.  
PR 20-NOV-1998; 98US-109304P.  
PR 23-MAR-1999; 99US-125778P.  
PR 15-JUN-1999; 99US-139695P.  
PR 20-JUL-1999; 99US-145070P.  
PR 26-JUL-1999; 99US-145698P.  
PR 17-AUG-1999; 99US-149396P.  
PR 07-DEC-1999; 99US-169495P.  
PR 15-NOV-2001; 2001US-0002796.

XX

PA (GETH ) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;  
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;  
PI Wood WI, Zhang Z;

XX

DR WPI; 2003-328482/31.

DR N-PSDB; ACA60458.

XX

PT Novel secreted and transmembrane polypeptide for modulating biological  
PT activity of cell expressing the polypeptide, for identifying agonists  
PT or antagonists of polypeptide, and as molecular weight markers -

XX

PS Claim 12; Fig 10; 254pp; English.

XX

CC The invention describes an isolated, secreted and transmembrane  
CC polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP  
CC (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337,  
CC PRO1411, PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor  
CC receptor (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630,  
CC PRO265 or PRO951 polypeptide, and for linking a bioactive molecule to a  
CC cell expressing the above polypeptides. The bioactive molecule, a toxin,  
CC radiolabel or an antibody, causes cell death. PRO is useful in assays to  
CC identify other proteins or molecules involved in binding interaction.  
CC The polynucleotide (II) encoding (I) is useful in chromosome and gene  
CC mapping, in generation of antisense RNA and DNA, for generating  
CC transgenic animals or knockout animals which in turn are useful in the  
CC development and screening of therapeutically useful reagents, to  
CC construct hybridisation probes for mapping the gene which encodes the  
CC PRO and for the genetic analysis of individuals with genetic disorders,  
CC in gene therapy, for chromosome identification and as a chromosome  
CC marker. (I) and (II) are useful for tissue typing. This is the amino  
CC acid sequence of a novel human secreted and transmembrane PRO  
CC polypeptide.



SQ Sequence 448 AA;

Query Match 99.8%; Score 2527; DB 24; Length 448;  
Best Local Similarity 99.8%; Pred. No. 9.9e-159;  
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MPGIKRILTVTII LALCLPSFGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV	60
Db	1	MPGIKRILTVTII LALCLPSFGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV	60
Qy	61	NQNGGYLCIPRTNPVYRGPSYNPYSTPYSGPYPAAPPLSAPNYPTISRPICRFGYQMD	120
Db	61	NQNGGYLCIPRTNPVYRGPSYNPYSTPYSGPYPAAPPLSAPNYPTISRPICRFGYQMD	120
Qy	121	ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCSDGYWLLGQCLDIDECRYGYCQQL	180
Db	121	ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCSDGYWLLGQCLDIDECRYGYCQQL	180
Qy	181	CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE	240
Db	181	CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE	240
Qy	241	DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN	300
Db	241	DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN	300
Qy	301	LQQTCTYNLQGGFKCIDPIRCEBEPYLISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS	360
Db	301	LQQTCTYNLQGGFKCIDPIRCEBEPYLISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS	360
Qy	361	VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQDL	420
Db	361	VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQDL	420
Qy	421	EMITVNTVINFRGSSVIRLRIYVSOYFF 448	
Db	421	EMITVNTVINFRGSSVIRLRIYVSOYFF 448	

## ABU65772

ID   ABU65772 standard; Protein; 448 AA.

AC ABU65772;

DT

DE

KW

KW

KW

XX

OS Homo sapiens.  
XX  
PN US2003036156-A1.  
XX  
PD 20-FEB-2003.  
XX  
PF 02-JUL-2002; 2002US-0188767.  
XX  
PR 16-SEP-1998; 98WO-US19330.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 08-MAR-1999; 99WO-US05028.  
PR 14-MAY-1999; 99WO-US10733.  
PR 02-JUN-1999; 99WO-US12252.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 01-DEC-1999; 99WO-US28301.  
PR 02-DEC-1999; 99WO-US28551.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 29-AUG-2001; 2001WO-US27099.  
PR 18-SEP-1997; 97US-059263P.  
PR 18-SEP-1997; 97US-059266P.  
PR 17-OCT-1997; 97US-062250P.  
PR 21-OCT-1997; 97US-063486P.  
PR 24-OCT-1997; 97US-063120P.  
PR 24-OCT-1997; 97US-063121P.  
PR 28-OCT-1997; 97US-063540P.  
PR 28-OCT-1997; 97US-063541P.  
PR 28-OCT-1997; 97US-063544P.  
PR 28-OCT-1997; 97US-063564P.  
PR 29-OCT-1997; 97US-063734P.  
PR 31-OCT-1997; 97US-063870P.  
PR 31-OCT-1997; 97US-064103P.  
PR 13-NOV-1997; 97US-065311P.

PR	21-NOV-1997;	97US-066120P.
PR	24-NOV-1997;	97US-066466P.
PR	24-NOV-1997;	97US-066772P.
PR	11-DEC-1997;	97US-069335P.
PR	12-DEC-1997;	97US-069425P.
PR	17-DEC-1997;	97US-069870P.
PR	18-DEC-1997;	97US-068017P.
PR	10-MAR-1998;	98US-077450P.
PR	11-MAR-1998;	98US-077632P.
PR	11-MAR-1998;	98US-077649P.
PR	20-MAR-1998;	98US-078886P.
PR	20-MAR-1998;	98US-078939P.
PR	27-MAR-1998;	98US-079664P.
PR	27-MAR-1998;	98US-079786P.
PR	31-MAR-1998;	98US-080107P.
PR	31-MAR-1998;	98US-080194P.
PR	01-APR-1998;	98US-080327P.
PR	01-APR-1998;	98US-080333P.
PR	08-APR-1998;	98US-081049P.
PR	08-APR-1998;	98US-081070P.
PR	09-APR-1998;	98US-081195P.
PR	15-APR-1998;	98US-081838P.
PR	21-APR-1998;	98US-082568P.
PR	21-APR-1998;	98US-082569P.
PR	22-APR-1998;	98US-082704P.
PR	22-APR-1998;	98US-082797P.
PR	28-APR-1998;	98US-083322P.
PR	29-APR-1998;	98US-083495P.
PR	29-APR-1998;	98US-083496P.
PR	29-APR-1998;	98US-083499P.
PR	29-APR-1998;	98US-083559P.
PR	05-MAY-1998;	98US-084366P.
PR	06-MAY-1998;	98US-084414P.
PR	07-MAY-1998;	98US-084639P.
PR	07-MAY-1998;	98US-084640P.
PR	07-MAY-1998;	98US-084643P.
PR	15-MAY-1998;	98US-085579P.
PR	15-MAY-1998;	98US-085580P.
PR	15-MAY-1998;	98US-085582P.
PR	15-MAY-1998;	98US-085700P.
PR	18-MAY-1998;	98US-086023P.
PR	22-MAY-1998;	98US-086392P.
PR	22-MAY-1998;	98US-086486P.
PR	28-MAY-1998;	98US-087098P.
PR	28-MAY-1998;	98US-087208P.
PR	02-JUN-1998;	98US-087609P.
PR	02-JUN-1998;	98US-087759P.
PR	03-JUN-1998;	98US-087827P.
PR	04-JUN-1998;	98US-088025P.
PR	04-JUN-1998;	98US-088028P.
PR	04-JUN-1998;	98US-088029P.
PR	04-JUN-1998;	98US-088033P.
PR	04-JUN-1998;	98US-088326P.
PR	05-JUN-1998;	98US-088167P.
PR	05-JUN-1998;	98US-088202P.
PR	05-JUN-1998;	98US-088212P.
PR	05-JUN-1998;	98US-088217P.

PR	09-JUN-1998;	98US-088655P.
PR	10-JUN-1998;	98US-088722P.
PR	10-JUN-1998;	98US-088738P.
PR	10-JUN-1998;	98US-088740P.
PR	10-JUN-1998;	98US-088811P.
PR	10-JUN-1998;	98US-088824P.
PR	10-JUN-1998;	98US-088825P.
PR	10-JUN-1998;	98US-088826P.
PR	11-JUN-1998;	98US-088861P.
PR	11-JUN-1998;	98US-088863P.
PR	11-JUN-1998;	98US-088876P.
PR	12-JUN-1998;	98US-089090P.
PR	12-JUN-1998;	98US-089105P.
PR	16-JUN-1998;	98US-089512P.
PR	16-JUN-1998;	98US-089514P.
PR	17-JUN-1998;	98US-089538P.
PR	17-JUN-1998;	98US-089598P.
PR	17-JUN-1998;	98US-089653P.
PR	18-JUN-1998;	98US-089908P.
PR	19-JUN-1998;	98US-089952P.
PR	22-JUN-1998;	98US-090246P.
PR	22-JUN-1998;	98US-090252P.
PR	22-JUN-1998;	98US-090254P.
PR	24-JUN-1998;	98US-090429P.
PR	24-JUN-1998;	98US-090435P.
PR	24-JUN-1998;	98US-090444P.
PR	24-JUN-1998;	98US-090461P.
PR	24-JUN-1998;	98US-090535P.
PR	24-JUN-1998;	98US-090540P.
PR	25-JUN-1998;	98US-090676P.
PR	25-JUN-1998;	98US-090678P.
PR	25-JUN-1998;	98US-090688P.
PR	25-JUN-1998;	98US-090690P.
PR	25-JUN-1998;	98US-090694P.
PR	25-JUN-1998;	98US-090695P.
PR	25-JUN-1998;	98US-090696P.
PR	26-JUN-1998;	98US-090862P.
PR	26-JUN-1998;	98US-090863P.
PR	26-JUN-1998;	98US-091010P.
PR	01-JUL-1998;	98US-091359P.
PR	01-JUL-1998;	98US-091544P.
PR	02-JUL-1998;	98US-091478P.
PR	02-JUL-1998;	98US-091486P.
PR	02-JUL-1998;	98US-091626P.
PR	02-JUL-1998;	98US-091628P.
PR	02-JUL-1998;	98US-091632P.
PR	24-JUL-1998;	98US-094006P.
PR	04-AUG-1998;	98US-095282P.
PR	10-AUG-1998;	98US-095998P.
PR	10-AUG-1998;	98US-096012P.
PR	17-AUG-1998;	98US-096757P.
PR	17-AUG-1998;	98US-096766P.
PR	17-AUG-1998;	98US-096867P.
PR	17-AUG-1998;	98US-096891P.
PR	17-AUG-1998;	98US-096897P.
PR	18-AUG-1998;	98US-096949P.
PR	18-AUG-1998;	98US-096959P.

PR 18-AUG-1998; 98US-097022P.  
 PR 26-AUG-1998; 98US-097952P.  
 PR 26-AUG-1998; 98US-097954P.  
 PR 26-AUG-1998; 98US-097955P.  
 PR 26-AUG-1998; 98US-097971P.  
 PR 26-AUG-1998; 98US-097974P.  
 PR 26-AUG-1998; 98US-098014P.  
 PR 01-SEP-1998; 98US-098716P.  
 PR 01-SEP-1998; 98US-098723P.  
 PR 02-SEP-1998; 98US-098803P.  
 PR 02-SEP-1998; 98US-098821P.  
 PR 02-SEP-1998; 98US-098843P.  
 PR 09-SEP-1998; 98US-099602P.  
 PR 10-SEP-1998; 98US-099741P.

Query Match 99.8%; Score 2527; DB 24; Length 448;  
 Best Local Similarity 99.8%; Pred. No. 9.9e-159;  
 Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy      1  MPGIKRILTVTILALCLSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
      |||
Db      1  MPGIKRILTVTILALCLSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy      61  NQNGGYLCIPRTNPVYRGPYSNPYSTFYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD 120
      |||
Db      61  NQNGGYLCIPRTNPVYRGPYSNPYSTFYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy      121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSDTDGYWLLEGQCLDIDECRYGYCQQL 180
      |||
Db      121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSDTDGYWLLEGQCLDIDECRYGYCQQL 180

Qy      181  CANVPGSYSCTCNPGFITLNEGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
      |||
Db      181  CANVPGSYSCTCNPGFITLNEGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy      241  DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
      |||
Db      241  DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

Qy      301  LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPPTILYRDMDVVSGRS 360
      |||
Db      301  LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPPTILYRDMDVVSGRS 360

Qy      361  VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
      |||
Db      361  VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420

Qy      421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
      |||
Db      421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
  
```

RESULT 14

ABU66105

ID ABU66105 standard; Protein; 448 AA.

XX

AC ABU66105;

XX  
DT 20-MAY-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO210.  
XX  
KW Human; secreted protein; transmembrane protein; cytostatic;  
KW gene Therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;  
KW adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.  
XX  
OS Homo sapiens.  
XX  
PN US2003036157-A1.  
XX  
PD 20-FEB-2003.  
XX  
PF 02-JUL-2002; 2002US-0188769.  
XX  
PR 16-SEP-1998; 98WO-US19330.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 08-MAR-1999; 99WO-US05028.  
PR 14-MAY-1999; 99WO-US10733.  
PR 02-JUN-1999; 99WO-US12252.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 01-DEC-1999; 99WO-US28301.  
PR 02-DEC-1999; 99WO-US28551.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 29-AUG-2001; 2001WO-US27099.  
PR 18-SEP-1997; 97US-059263P.  
PR 18-SEP-1997; 97US-059266P.  
PR 17-OCT-1997; 97US-062250P.  
PR 21-OCT-1997; 97US-063486P.

PR	24-OCT-1997;	97US-063120P.
PR	24-OCT-1997;	97US-063121P.
PR	28-OCT-1997;	97US-063540P.
PR	28-OCT-1997;	97US-063541P.
PR	28-OCT-1997;	97US-063544P.
PR	28-OCT-1997;	97US-063564P.
PR	29-OCT-1997;	97US-063734P.
PR	31-OCT-1997;	97US-063870P.
PR	31-OCT-1997;	97US-064103P.
PR	13-NOV-1997;	97US-065311P.
PR	21-NOV-1997;	97US-066120P.
PR	24-NOV-1997;	97US-066466P.
PR	24-NOV-1997;	97US-066772P.
PR	11-DEC-1997;	97US-069335P.
PR	12-DEC-1997;	97US-069425P.
PR	17-DEC-1997;	97US-069870P.
PR	18-DEC-1997;	97US-068017P.
PR	10-MAR-1998;	98US-077450P.
PR	11-MAR-1998;	98US-077632P.
PR	11-MAR-1998;	98US-077649P.
PR	20-MAR-1998;	98US-078886P.
PR	20-MAR-1998;	98US-078939P.
PR	27-MAR-1998;	98US-079664P.
PR	27-MAR-1998;	98US-079786P.
PR	31-MAR-1998;	98US-080107P.
PR	31-MAR-1998;	98US-080194P.
PR	01-APR-1998;	98US-080327P.
PR	01-APR-1998;	98US-080333P.
PR	08-APR-1998;	98US-081049P.
PR	08-APR-1998;	98US-081070P.
PR	09-APR-1998;	98US-081195P.
PR	15-APR-1998;	98US-081838P.
PR	21-APR-1998;	98US-082568P.
PR	21-APR-1998;	98US-082569P.
PR	22-APR-1998;	98US-082704P.
PR	22-APR-1998;	98US-082797P.
PR	28-APR-1998;	98US-083322P.
PR	29-APR-1998;	98US-083495P.
PR	29-APR-1998;	98US-083496P.
PR	29-APR-1998;	98US-083499P.
PR	29-APR-1998;	98US-083559P.
PR	05-MAY-1998;	98US-084366P.
PR	06-MAY-1998;	98US-084414P.
PR	07-MAY-1998;	98US-084639P.
PR	07-MAY-1998;	98US-084640P.
PR	07-MAY-1998;	98US-084643P.
PR	15-MAY-1998;	98US-085579P.
PR	15-MAY-1998;	98US-085580P.
PR	15-MAY-1998;	98US-085582P.
PR	15-MAY-1998;	98US-085700P.
PR	18-MAY-1998;	98US-086023P.
PR	22-MAY-1998;	98US-086392P.
PR	22-MAY-1998;	98US-086486P.
PR	28-MAY-1998;	98US-087098P.
PR	28-MAY-1998;	98US-087208P.
PR	02-JUN-1998;	98US-087609P.
PR	02-JUN-1998;	98US-087759P.

PR	03-JUN-1998;	98US-087827P.
PR	04-JUN-1998;	98US-088025P.
PR	04-JUN-1998;	98US-088028P.
PR	04-JUN-1998;	98US-088029P.
PR	04-JUN-1998;	98US-088033P.
PR	04-JUN-1998;	98US-088326P.
PR	05-JUN-1998;	98US-088167P.
PR	05-JUN-1998;	98US-088202P.
PR	05-JUN-1998;	98US-088212P.
PR	05-JUN-1998;	98US-088217P.
PR	09-JUN-1998;	98US-088655P.
PR	10-JUN-1998;	98US-088722P.
PR	10-JUN-1998;	98US-088738P.
PR	10-JUN-1998;	98US-088740P.
PR	10-JUN-1998;	98US-088811P.
PR	10-JUN-1998;	98US-088824P.
PR	10-JUN-1998;	98US-088825P.
PR	10-JUN-1998;	98US-088826P.
PR	11-JUN-1998;	98US-088861P.
PR	11-JUN-1998;	98US-088863P.
PR	11-JUN-1998;	98US-088876P.
PR	12-JUN-1998;	98US-089090P.
PR	12-JUN-1998;	98US-089105P.
PR	16-JUN-1998;	98US-089512P.
PR	16-JUN-1998;	98US-089514P.
PR	17-JUN-1998;	98US-089538P.
PR	17-JUN-1998;	98US-089598P.
PR	17-JUN-1998;	98US-089653P.
PR	18-JUN-1998;	98US-089908P.
PR	19-JUN-1998;	98US-089952P.
PR	22-JUN-1998;	98US-090246P.
PR	22-JUN-1998;	98US-090252P.
PR	22-JUN-1998;	98US-090254P.
PR	24-JUN-1998;	98US-090429P.
PR	24-JUN-1998;	98US-090435P.
PR	24-JUN-1998;	98US-090444P.
PR	24-JUN-1998;	98US-090461P.
PR	24-JUN-1998;	98US-090535P.
PR	24-JUN-1998;	98US-090540P.
PR	25-JUN-1998;	98US-090676P.
PR	25-JUN-1998;	98US-090678P.
PR	25-JUN-1998;	98US-090688P.
PR	25-JUN-1998;	98US-090690P.
PR	25-JUN-1998;	98US-090694P.
PR	25-JUN-1998;	98US-090695P.
PR	25-JUN-1998;	98US-090696P.
PR	26-JUN-1998;	98US-090862P.
PR	26-JUN-1998;	98US-090863P.
PR	26-JUN-1998;	98US-091010P.
PR	01-JUL-1998;	98US-091359P.
PR	01-JUL-1998;	98US-091544P.
PR	02-JUL-1998;	98US-091478P.
PR	02-JUL-1998;	98US-091486P.
PR	02-JUL-1998;	98US-091626P.
PR	02-JUL-1998;	98US-091628P.
PR	02-JUL-1998;	98US-091632P.
PR	24-JUL-1998;	98US-094006P.



PR 04-AUG-1998; 98US-095282P.  
 PR 10-AUG-1998; 98US-095998P.  
 PR 10-AUG-1998; 98US-096012P.  
 PR 17-AUG-1998; 98US-096757P.  
 PR 17-AUG-1998; 98US-096766P.  
 PR 17-AUG-1998; 98US-096867P.  
 PR 17-AUG-1998; 98US-096891P.  
 PR 17-AUG-1998; 98US-096897P.  
 PR 18-AUG-1998; 98US-096949P.  
 PR 18-AUG-1998; 98US-096959P.  
 PR 18-AUG-1998; 98US-097022P.  
 PR 26-AUG-1998; 98US-097952P.  
 PR 26-AUG-1998; 98US-097954P.  
 PR 26-AUG-1998; 98US-097955P.  
 PR 26-AUG-1998; 98US-097971P.  
 PR 26-AUG-1998; 98US-097974P.  
 PR 26-AUG-1998; 98US-098014P.  
 PR 01-SEP-1998; 98US-098716P.  
 PR 01-SEP-1998; 98US-098723P.  
 PR 02-SEP-1998; 98US-098803P.  
 PR 02-SEP-1998; 98US-098821P.  
 PR 02-SEP-1998; 98US-098843P.  
 PR 09-SEP-1998; 98US-099602P.  
 PR 10-SEP-1998; 98US-099741P.  
 PR 10-SEP-1998; 98US-099754P.  
 PR 10-SEP-1998; 98US-099763P.

Query Match 99.8%; Score 2527; DB 24; Length 448;  
 Best Local Similarity 99.8%; Pred. No. 9.9e-159;  
 Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPGIKRILTVTILALCLPSGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60  
 |||||  
 Db 1 MPGIKRILTVTILALCLPSGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60  
 |||||  
 Qy 61 NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120  
 |||||  
 Db 61 NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120  
 |||||  
 Qy 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCDGYWLLLEGQCLDIDECRYGYCQQL 180  
 |||||  
 Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCDGYWLLLEGQCLDIDECRYGYCQQL 180  
 |||||  
 Qy 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNITYGSFICRCDPGYELEE 240  
 |||||  
 Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNITYGSLICRCDPGYELEE 240  
 |||||  
 Qy 241 DGVHCSMDDECSFSSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |||||  
 Db 241 DGVHCSMDDECSFSSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |||||  
 Qy 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRMDMVVSGRS 360  
 |||||  
 Db 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRMDMVVSGRS 360  
 |||||  
 Qy 361 VPADIFQMQAATTPYGYIYFOIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420  
 |||||

Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQDL 420  
 QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448  
 |||||  
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 15

ABU67141

ID ABU67141 standard; Protein; 448 AA.

XX

AC ABU67141;

XX

DT 28-MAY-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO210.

XX

KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533;  
 KW PRO301; PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003;  
 KW PRO6004; PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;  
 KW fibroblast growth factor receptor; cell death; chromosome mapping;  
 KW gene mapping; transgenic animal; knockout animal; gene therapy;  
 KW tumour; obesity; diabetes; insulinaemia; vascular permeability;  
 KW cardiac insufficiency disorder; immune response; hearing loss;  
 KW auditory hair cell regeneration; bone disorder; cartilage disorder;  
 KW sports injury; arthritis.

XX

OS Homo sapiens.

XX

PN US2003032062-A1.

XX

PD 13-FEB-2003.

XX

PF 01-FEB-2002; 2002US-0066273.

XX

PR 14-JUL-1998; 98WO-US14552.

PR 10-SEP-1998; 98WO-US18824.

PR 14-SEP-1998; 98WO-US19093.

PR 16-SEP-1998; 98WO-US19330.

PR 17-SEP-1998; 98WO-US19437.

PR 20-NOV-1998; 98WO-US24855.

PR 25-NOV-1998; 98WO-US25190.

PR 01-DEC-1998; 98WO-US25108.

PR 08-MAR-1999; 99WO-US05028.

PR 02-JUN-1999; 99WO-US12252.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28301.

PR 02-DEC-1999; 99WO-US28565.

PR 20-DEC-1999; 99WO-US30999.

PR 05-JAN-2000; 2000WO-US00219.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 09-MAR-2000; 2000WO-US06471.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 26-AUG-1997; 97US-056974P.  
PR 17-SEP-1997; 97US-059115P.  
PR 18-SEP-1997; 97US-059263P.  
PR 19-SEP-1997; 97US-059588P.  
PR 17-OCT-1997; 97US-062285P.  
PR 24-OCT-1997; 97US-062816P.  
PR 24-OCT-1997; 97US-063082P.  
PR 27-OCT-1997; 97US-063329P.  
PR 29-OCT-1997; 97US-063733P.  
PR 21-NOV-1997; 97US-066364P.  
PR 25-NOV-1997; 97US-066840P.  
PR 16-DEC-1997; 97US-069694P.  
PR 09-FEB-1998; 98US-074086P.  
PR 09-FEB-1998; 98US-074092P.  
PR 25-MAR-1998; 98US-079294P.  
PR 08-APR-1998; 98US-081049P.  
PR 10-AUG-1998; 98US-095998P.  
PR 18-AUG-1998; 98US-097000P.  
PR 09-SEP-1998; 98US-099601P.  
PR 10-SEP-1998; 98US-099803P.  
PR 10-SEP-1998; 98US-099811P.  
PR 10-SEP-1998; 98US-099812P.  
PR 17-SEP-1998; 98US-100858P.  
PR 24-SEP-1998; 98US-101922P.  
PR 28-OCT-1998; 98US-106032P.  
PR 20-NOV-1998; 98US-109304P.  
PR 23-MAR-1999; 99US-125778P.  
PR 15-JUN-1999; 99US-139695P.  
PR 20-JUL-1999; 99US-145070P.  
PR 26-JUL-1999; 99US-145698P.  
PR 17-AUG-1999; 99US-149396P.  
PR 07-DEC-1999; 99US-169495P.  
PR 15-NOV-2001; 2001US-0002796.

XX

(GETH ) GENENTECH INC.

PA

XX

PI

Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;



Db	181		CANVPGSYSC	TCNPGFTLN	EDGRSCQD	VNECATEN	PCVQTCV	NTYGS	LI	CRCD	PGYELEE	240	
Qy	241		DGVHCS	DMDECS	FSFELC	QHECVN	QPGTYF	CS	CPPGYILL	DDNRSC	DINECE	HRNHTCN 300	
Db	241		DGVHCS	DMDECS	FSFELC	QHECVN	QPGTYF	CS	CPPGYILL	DDNRSC	DINECE	HRNHTCN 300	
Qy	301		LQQT	CYNL	QGGFKC	IDPIR	CEPYLR	ISDN	RCMCPA	ENPGCRD	QPF	TILYRDM	DVVSGRS 360
Db	301		LQQT	CYNL	QGGFKC	IDPIR	CEPYLR	ISDN	RCMCPA	ENPGCRD	QPF	TILYRDM	DVVSGRS 360
Qy	361		VPAD	IFQM	QATTRY	PGAYYI	IFQIK	SGNE	GREFYM	RQTGP	ISATL	VMTRPI	KGP
Db	361		VPAD	IFQM	QATTRY	PGAYYI	IFQIK	SGNE	GREFYM	RQTGP	ISATL	VMTRPI	KGP
Qy	421		EMIT	VNTVIN	FRGSSV	IRLRIY	VSQY	PF	448				
Db	421		EMIT	VNTVIN	FRGSSV	IRLRIY	VSQY	PF	448				

Search completed: January 9, 2004, 12:33:33

Job time : 41.6051 secs

OM protein - protein search, using sw model

Run on: January 9, 2004, 12:30:17 ; Search time 15.9449 Seconds  
(without alignments)  
1188.799 Million cell updates/sec

Title: US-09-674-379A-13  
Perfect score: 2533  
Sequence: 1 MPGIKRILTVTILALCLPSP.....INFRGSSVIRLRIVVSQYPF 448

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2533	100.0	448	2	US-08-884-072-1	Sequence 1, Appli
2	2533	100.0	448	4	US-09-212-168-1	Sequence 1, Appli
3	1827	72.1	335	4	US-09-312-283C-186	Sequence 186, App
4	1791	70.7	337	3	US-09-188-930-186	Sequence 186, App
5	1289	50.9	443	2	US-08-833-963C-2	Sequence 2, Appli
6	1289	50.9	443	3	US-08-980-514-1	Sequence 1, Appli
7	963.5	38.0	387	2	US-08-884-072-5	Sequence 5, Appli
8	963.5	38.0	387	2	US-08-833-963C-9	Sequence 9, Appli
9	963.5	38.0	387	3	US-08-980-514-3	Sequence 3, Appli
10	963.5	38.0	387	4	US-09-212-168-5	Sequence 5, Appli
11	912.5	36.0	274	3	US-09-188-930-336	Sequence 336, App

12	912.5	36.0	274	4	US-09-312-283C-336	Sequence 336, App
13	544	21.5	1394	6	5177197-30	Patent No. 5177197
14	521.5	20.6	575	4	US-09-482-273-159	Sequence 159, App
15	521.5	20.6	638	4	US-09-482-273-245	Sequence 245, App
16	475	18.8	638	2	US-08-897-443-1	Sequence 1, Appli
17	463	18.3	1833	3	US-08-479-722B-2	Sequence 2, Appli
18	463	18.3	1833	5	PCT-US95-02251-18	Sequence 18, Appl
19	461	18.2	1251	5	PCT-US95-02251-3	Sequence 3, Appli
20	461	18.2	1252	1	US-08-199-780-3	Sequence 3, Appli
21	461	18.2	1252	2	US-08-316-650-3	Sequence 3, Appli
22	461	18.2	1253	3	US-08-479-722B-4	Sequence 4, Appli
23	452	17.8	956	2	US-08-897-443-3	Sequence 3, Appli
24	392	15.5	886	3	US-09-110-116-3	Sequence 3, Appli
25	389.5	15.4	353	4	US-09-482-273-243	Sequence 243, App
26	377	14.9	2471	1	US-08-185-432-16	Sequence 16, Appl
27	377	14.9	2471	1	US-08-083-590A-19	Sequence 19, Appl
28	377	14.9	2471	3	US-08-532-384-19	Sequence 19, Appl
29	377	14.9	2471	4	US-08-899-232-1	Sequence 1, Appli
30	375	14.8	810	2	US-08-820-170A-34	Sequence 34, Appl
31	375	14.8	810	3	US-09-055-699-34	Sequence 34, Appl
32	375	14.8	810	3	US-09-273-565-34	Sequence 34, Appl
33	375	14.8	810	4	US-09-565-538-34	Sequence 34, Appl
34	375	14.8	810	4	US-09-661-468-34	Sequence 34, Appl
35	375	14.8	810	4	US-09-976-165-34	Sequence 34, Appl
36	366	14.4	816	2	US-08-820-170A-37	Sequence 37, Appl
37	366	14.4	816	3	US-09-055-699-37	Sequence 37, Appl
38	366	14.4	816	3	US-09-273-565-37	Sequence 37, Appl
39	366	14.4	816	4	US-09-565-538-37	Sequence 37, Appl
40	366	14.4	816	4	US-09-661-468-37	Sequence 37, Appl
41	366	14.4	816	4	US-09-976-165-37	Sequence 37, Appl
42	360.5	14.2	1964	4	US-09-467-997-1	Sequence 1, Appli
43	359	14.2	2703	1	US-08-185-432-19	Sequence 19, Appl
44	359	14.2	2703	4	US-08-899-232-4	Sequence 4, Appli
45	350.5	13.8	652	2	US-08-751-305-2	Sequence 2, Appli

#### ALIGNMENTS

#### RESULT 1

US-08-884-072-1

; Sequence 1, Application US/08884072

; Patent No. 5872234

#### ; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

; NUMBER OF SEQUENCES: 6

#### ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,072
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0333 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CORNNOT01
; CLONE: 45517
;
US-08-884-072-1

```

```

Query Match          100.0%; Score 2533; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.2e-193;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1  MPGIKRILTVTILALCLPSGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
Db      1  MPGIKRILTVTILALCLPSGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61  NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGGPYPAAAPLSAPNYPTISRPLICRFGYQMD 120
Db     61  NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGGPYPAAAPLSAPNYPTISRPLICRFGYQMD 120

Qy    121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLBGQCLDIDECRYGYCQQL 180
Db    121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLBGQCLDIDECRYGYCQQL 180

Qy    181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNITYGSFICRCDPGYELEE 240
Db    181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNITYGSFICRCDPGYELEE 240

Qy    241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300
Db    241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300

Qy    301  LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS 360
Db    301  LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS 360

```



QY 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTMRIKGPRIQLDL 420  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTMRIKGPRIQLDL 420  
 ||||||||||||||||||||||||||||||||||||||||  
 QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448  
 ||||||||||||||||||||||||||||  
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 2

US-09-212-168-1

; Sequence 1, Application US/09212168

; Patent No. 6303765

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/212,168

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/884,072

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0333 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 448 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: CORNNOT01

; CLONE: 45517

US-09-212-168-1

Query Match 100.0%; Score 2533; DB 4; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-193;  
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
      |||
Db      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61  NQNGGYLCIPRTNPFVYRGPYSNPYSTPYSGPYAAAPLSAPNYPTISRPLICRFGYQMD 120
      |||
Db     61  NQNGGYLCIPRTNPFVYRGPYSNPYSTPYSGPYAAAPLSAPNYPTISRPLICRFGYQMD 120

Qy    121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCDTGYNWLEGGQCLDIDECRYGYCQQL 180
      |||
Db    121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCDTGYNWLEGGQCLDIDECRYGYCQQL 180

Qy    181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSPICRCDPGYLEEE 240
      |||
Db    181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSPICRCDPGYLEEE 240

Qy    241  DGVHCSMDDECSPSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300
      |||
Db    241  DGVHCSMDDECSPSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300

Qy    301  LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPTTILYRDMDVVSGRS 360
      |||
Db    301  LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPTTILYRDMDVVSGRS 360

Qy    361  VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPICKGPREIQLDL 420
      |||
Db    361  VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPICKGPREIQLDL 420

Qy    421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
      |||
Db    421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
  
```

### RESULT 3

US-09-312-283C-186  
 ; Sequence 186, Application US/09312283C  
 ; Patent No. 6573095  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Watson, James D.  
 ; APPLICANT: Strachan, Lorna  
 ; APPLICANT: Sleeman, Matthew  
 ; APPLICANT: Onrust, Rene  
 ; APPLICANT: Murison, James G.  
 ; APPLICANT: Kumble, Krishanand D.  
 ; TITLE OF INVENTION: Compositions Isolated from Skin Cells  
 ; TITLE OF INVENTION: and Methods for Their Use  
 ; FILE REFERENCE: 11000.1011c2  
 ; CURRENT APPLICATION NUMBER: US/09/312,283C  
 ; CURRENT FILING DATE: 1999-05-14  
 ; NUMBER OF SEQ ID NOS: 425  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 186

; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-312-283C-186

Query Match 72.1%; Score 1827; DB 4; Length 335;  
Best Local Similarity 95.2%; Pred. No. 2.1e-137;  
Matches 319; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

```
QY      114 RFGYQMDESNCQVDVDECATDSHCNFTQICINTEGGYTCSCTDGYWLEGGCCLDIDECR 173
      |||
DB      1 RFGYQMDEGNQCVDVDECATDSHCNFTQICINTEGGYTCSCTDGYWLEGGCCLDIDECR 60
      |||

QY      174 YGYCQQLCANVPGSYSCTCNPGFTLNEDGRSQDVNECATENPCVQTCVNTYGSFICRCD 233
      |||
DB      61 YGYCQQLCANVPGSYSCTCNPGFTLNEDGRSQDVNECATENPCVQTCVNTYGSFICRCD 120
      |||

QY      234 PGYELEEDGVHCSMDDECSFSEFLCQHECVNPGTYFCSCPPGYILLDNRSQDINECE 293
      |||
DB      121 PGYELEEDGIHCSMDDECSFSEFLCQHECVNPGSYFCSCPPGYVLLDNRSQDINECE 180
      |||

QY      294 HRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRIISDNRCMCPAENPGCRDQFFTILYRDM 353
      |||
DB      181 HRNHTCTPLQTCYNLQGGFKCIDPIVCEEPYLLIGDNRCMCPAENTGCRDQFFTILFRDM 240
      |||

QY      354 DVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGF 413
      |||
DB      241 DVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGF 300
      |||

QY      414 REIQLDLEMITVMTVINFRGSSVIRLRIYVSQYPF 448
      |||
DB      301 RDIQLDLEMITVMTVINFRGSSVIRLRIYVSQYPF 335
      |||
```

RESULT 4

US-09-188-930-186  
; Sequence 186, Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James Greg  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; TITLE OF INVENTION: and Methods For Their Use  
; FILE REFERENCE: 11000.1011c1  
; CURRENT APPLICATION NUMBER: US/09/188,930A  
; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 186  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Rat  
; FEATURE:  
; NAME/KEY: UNSURE





Db 351 TSERSVPADVFQIQATSVYPGAYNAFQIRAGNSQGDVFYIRQINNVSAMLVLARPVTGPRE 410  
 QY 416 IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448  
 Db 411 YVLDLEMTMNSLSYRASSVLRLTVFVGAYTF 443

RESULT 6

US-08-980-514-1

; Sequence 1, Application US/08980514

; Patent No. 6004753

; GENERAL INFORMATION:

; APPLICANT: Yue, Henry

; APPLICANT: Guegler, Karl J.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: HUMAN S1-5-ECMP-LIKE PROT

; TITLE OF INVENTION: E1N

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Dr.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/980,514

; FILING DATE: Filed Herewith

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0436 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 443 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: BRSTNOT13

; CLONE: 2786449

US-08-980-514-1

Query Match 50.9%; Score 1289; DB 3; Length 443;  
 Best Local Similarity 49.9%; Pred. No. 1.3e-94;

Matches 226; Conservative 74; Mismatches 131; Indels 22; Gaps 5;

### RESULT 7

; Sequence 5, Application US/08884072

GENERAL INFORMATION:

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,072
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0333 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 458228
US-08-884-072-5

```

```

Query Match          38.0%; Score 963.5; DB 2; Length 387;
Best Local Similarity 48.3%; Pred. No. 7.3e-69;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

```

```

Qy      96 APPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICINTEGGYTCS 155
      | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy      156 TDGYWLLEGGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE 214
      | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      96 PPGYQKRGRQCVDI DECTIPPYCHQRCVNTPGSFYQCSPGFQLAANNYTCDVINECDAS 155

Qy      215 NPCVQTCVNTYGSFICRCDPGYEEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCP 274
      | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      156 NQCAQQCYNII LGSFICQCNQGYELSSDRINCBEDI DECTRSSYLCCQYQCVCNEPFGKFCMCP 215

Qy      275 PGYILLDDNRSQDINECEHRNHTCNLQQTCCYNLGGGFKCIDPIRCEEPYLRISDNRCMC 334
      | | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      216 QGYQVV--RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPRNPQDPPYILTPENRCVC 273

Qy      335 PAENPGCRDQPFTILYRMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM 394
      | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      274 PVSNAMCRELPQSIYVKYSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGEBFYL 333

Qy      395 RQTGPISATLVMTPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
      | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      334 RQTSFVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLLTIIVGPFSP 387

```

```

RESULT 8
US-08-833-963C-9

```



```

; Sequence 9, Application US/08833963C
; Patent No. 5916769
; GENERAL INFORMATION:
; APPLICANT: Olsen, et al.
; TITLE OF INVENTION: Extracellular/Epidermal Growth Factor
; TITLE OF INVENTION: HCABA58X
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,963C
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/05033
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF258
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-963C-9

```

```

Query Match          38.0%; Score 963.5; DB 2; Length 387;
Best Local Similarity 48.3%; Pred. No. 7.3e-69;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

```

```

QY      96  APPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICINTEGGYTCS 155
      || | | : | | : | ||: | | | | : || | : | | | | : | |
Db      38  ADPQRIPSPNP--SHRIQCAAGYBQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

QY      156 TDGYWLLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE 214
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      96  PPGYQKRGBCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFLAANNYTCTVDINECDAS 155

QY      215 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDMECSFSEFLCQHECVNPGTYFCSCP 274
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      156 NQCAQQCYNILGSFICQCNQGYELSSDRLNCEIDEDCRTSSYLCCQYQCVNBPFGKFSMCP 215

```

QY 275 PGYILLDDNRSQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMC 334  
 || :: :||| ||| | | : ||| |||: |::||: :|||:  
 Db 216 QGYQVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFCYPRNPCQDPYILT PENRCVC 273  
 QY 335 PAENPGCRDQPFITILYRDM DVVSGRSPADIFQM QATTRYPGAYYIFQIKSGNEGREFYM 394  
 | | ||: | :||: | : | |||: |||: ||| | :||| |||:  
 Db 274 FVSNAMCRELPQSI VVKYMSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGFEYL 333  
 QY 395 RQTGPISATILVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448  
 ||| |:|| |::: ||| :|||: |||: || | |||: ||| : |  
 Db 334 RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFR TSSVLRLTIIVGPFSF 387

RESULT 9

US-08-980-514-3

; Sequence 3, Application US/08980514

; Patent No. 6004753

; GENERAL INFORMATION:

; APPLICANT: Yue, Henry

; APPLICANT: Guegler, Karl J.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: HUMAN S1-5-ECMP-LIKE PROT

; TITLE OF INVENTION: EIN

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Dr.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/980,514

; FILING DATE: Filed Herewith

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0436 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 387 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank  
; CLONE: 458228  
US-08-980-514-3

Query Match 38.0%; Score 963.5; DB 3; Length 387;  
Best Local Similarity 48.3%; Pred. No. 7.3e-69;  
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

```
Qy      96 APPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPTQICINTEGGYTCSC 155
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy      156 TDGYWLLLEGQCLDIDECRY-GYCQQLCANVPGSVSCTCNPGFTLNEDGRSCQDVNECATE 214
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYQCSPGFQLAANNYTCVDINECDAS 155

Qy      215 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSC 274
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      156 NQCAQQCYNILGSPICQCNQGYELSSDRLNCEBIDECRTSSYLQYQVCNEPGKPSMCP 215

Qy      275 PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMC 334
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      216 QGYQVW-RSRTCQDINECETTNE-CREDEMWNHYGGFRCPYPRNQDPYILTPEPNCVC 273

Qy      335 PAENFGCRDPQFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM 394
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      274 FVSNAMCRELPQSIYVYKYSIRSDRSVPDIFQIQATTIYANTINTFRIKSGNENGEPYL 333

Qy      395 RQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      334 RQTSFVSAMLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVRLRTIIVGPFSP 387
```

RESULT 10

US-09-212-168-5

; Sequence 5, Application US/09212168

; Patent No. 6303765

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/212,168

; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/884,072  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0333 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-855-0555  
 ; TELEFAX: 415-845-4166  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 387 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GenBank  
 ; CLONE: 458228  
 US-09-212-168-5

Query Match 38.0%; Score 963.5; DB 4; Length 387;  
 Best Local Similarity 48.3%; Pred. No. 7.3e-69;  
 Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

```

Qy      96 APPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICINTEGGYTCSC 155
      | | | | | : | | : | | | | | : | | | | | : | | | | | : | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy      156 TDGYWLLEGQCLDIDECRY-GYCOQLCANVPGSYSCNPGFTLNEDGRSCQDVNECATE 214
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYQCQSPGFQLAANNYTCVDINECDAS 155

Qy      215 NPCVQTCVNTYGSFICRCDPGYBLEEDGVHCSMDDECSFSEFLCQHECVNPGTYFCSCP 274
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      156 NQCAQQCYNILGSFICQCNQGYELSSDRLNCEIDIDECRTSSYLQCYQCVNEPGKPSCMCP 215

Qy      275 PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEBPYLRISDNRCMC 334
      | | : : | : | | | | | | | | | | | | | | | | | | | | | |
Db      216 QGYQVV-RSRTCQDINECETNE-CREDEMCWNYHGGFRCPYRNPQDPFYILTPENRVCV 273

Qy      335 PAENPGCRDPFTTILYRDMVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNREGFYFM 394
      | | | | | : | : | : | : | : | | | | | | | | | | | | | |
Db      274 PVSNAMECRELPQSIYKYMSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGIFYL 333

Qy      395 RQTGPISATLVMTRPKIGPREIQLDLEMITVMTVINFRGSSVIRLRIYVSQYPF 448
      | | | | | : : : | | | | | | | | | | | | | | | | | |
Db      334 RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTPRTSSVLRLLTIIVGPFPSF 387
  
```

RESULT 11  
 US-09-188-930-336  
 ; Sequence 336, Application US/09188930A  
 ; Patent No. 6150502

; GENERAL INFORMATION:  
 ; APPLICANT: Watson, James D.  
 ; APPLICANT: Strachan, Lorna  
 ; APPLICANT: Sleeman, Matthew  
 ; APPLICANT: Onrust, Rene  
 ; APPLICANT: Murison, James Greg  
 ; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
 ; TITLE OF INVENTION: and Methods For Their Use  
 ; FILE REFERENCE: 11000.1011c1  
 ; CURRENT APPLICATION NUMBER: US/09/188,930A  
 ; CURRENT FILING DATE: 1998-11-09  
 ; NUMBER OF SEQ ID NOS: 348  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 336  
 ; LENGTH: 274  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-09-188-930-336

Query Match 36.0%; Score 912.5; DB 3; Length 274;  
 Best Local Similarity 56.0%; Pred. No. 5.5e-65;  
 Matches 154; Conservative 47; Mismatches 73; Indels 1; Gaps 1;

```

Qy      174 YGYCQQLCANVPGSYSCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCD 233
        | ||| | :|||: | ||| | : ||| |||| | | | :|||:|:|
Db      1 YRYCQHRCNVLPGSFRCQCEPGFQLGFNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCH 60

Qy      234 PGYELEEDGVHSCDMDCESEFLCQHECVNPGTYFCSCPPGYILLDDNRSCQDINECE 293
        |||| | |||:|||||: |||: |||:| : ||| || | | |||:|
Db      61 QGYBLHRDGFSCSDIDECYSYSSYLCCQYRCVNEPGRFSCPCQGYQLL-ATRLCQDIDEC 119

Qy      294 HRNHTCNLQOTCYNLQGGFKCIDPIRCBEPYLIRISDNRCMPAENPGCRDPQFTILYRDM 353
        | |: ||| | |||:| | |||:|:|:| || | | | |:| |
Db      120 SGAHQCSEAQTCVNFHGGYRCVDINRCVEPYIQVSENRCCLPASNPLCREQPSIVHRYM 179

Qy      354 DVVSGRSVPADIFQMQATTYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 413
        : | |||||:|:|:| ||| |||:| | :||:| :|| |: |: ||
Db      180 TITERSVPADVPQIQATSVYPGAYNAFQIRAGNSQGDYFIQINNVSAMLVLARPVITGP 239

Qy      414 REIQLDLEMITVMTVINFRGSSVIRLRIYVSQYPF 448
        || |||||:|:|:| |||:| ||| | |
Db      240 REYVLDLEMTMNSLSMYRASSVLRLLTVFVGAYTF 274

```

# RESULT 12

US-09-312-283C-336  
 ; Sequence 336, Application US/09312283C  
 ; Patent No. 6573095  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Watson, James D.  
 ; APPLICANT: Strachan, Lorna  
 ; APPLICANT: Sleeman, Matthew  
 ; APPLICANT: Onrust, Rene  
 ; APPLICANT: Murison, James G.  
 ; APPLICANT: Kumble, Krishanand D.  
 ; TITLE OF INVENTION: Compositions Isolated from Skin Cells  
 ; TITLE OF INVENTION: and Methods for Their Use

; FILE REFERENCE: 11000.1011c2  
 ; CURRENT APPLICATION NUMBER: US/09/312,283C  
 ; CURRENT FILING DATE: 1999-05-14  
 ; NUMBER OF SEQ ID NOS: 425  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 336  
 ; LENGTH: 274  
 ; TYPE: PRT  
 ; ORGANISM: Mouse  
 US-09-312-283C-336

Query Match 36.0%; Score 912.5; DB 4; Length 274;  
 Best Local Similarity 56.0%; Pred. No. 5.5e-65;  
 Matches 154; Conservative 47; Mismatches 73; Indels 1; Gaps 1;

```

Qy      174 YGYCQQLCANVPGSYSCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCD 233
      | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1 YRYCQHRVCNVLPGSPRCQCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCH 60

Qy      234 PGYELEEDGVHCSMDMDECSFSEFLCQHECVNQPGTYFCSPPGYILLDDNRSCQDINECE 293
      |||| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      61 QGYELHRDGFSCSDIDECYSYSLCQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECE 119

Qy      294 HRNHTCNLQQTCTYNLQGGFKCIDPIRCEEPYLRIISDNRCMCPAENPGCRDQPFITLYRDM 353
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      120 SGAHQCEAQTCVNFHGGYRCVDITNRCVEPIYQVSENRCCLPASNPLCREQPSIVHRYM 179

Qy      354 DVVSGRSPVPADIPQMATTTRYPGAYYIFQIKSGNEGREFYMRQTFISATLVMTRPKGP 413
      : | ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      180 TITSEERSVPADVQIATSVVPGAYNAFQIRAGNSQGDIFYIRQINNVSAMLVLARPVGTG 239

Qy      414 REIQLDLEMITVMTVINFRGSSVIRLRIYVSQYPF 448
      || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      240 REYVLDELMTMNSLSYRASSVLRRLTVFVGAYTF 274
  
```

RESULT 13  
 5177197-30

; Patent No. 5177197

; APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;  
 ; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSEN-WELSH,  
 ; LENA; HELDIN, CARL-HENRIK

; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING  
 ; HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN

; NUMBER OF SEQUENCES: 53

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/487,343

; FILING DATE: 27-FEB-1990

; SEQ ID NO: 30:

; LENGTH: 1394

5177197-30

Query Match 21.5%; Score 544; DB 6; Length 1394;  
 Best Local Similarity 29.4%; Pred. No. 5.5e-35;  
 Matches 128; Conservative 52; Mismatches 134; Indels 122; Gaps 17;

```

Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMCMVNQNGGYLCIPRTNPFV 75
  
```

```

Db      562  CINLPVRYTCICYEGYRFSEQQRKCVDIDECTQVQHLC-SQGRCENTEGSFPLCI----- 614
Qy      76  YRGPYSNPYSTPYSGYPAAAPPLSAPNYPTISRPLI-----CRFGYQ 118
Db      615  -----CPAGFMASEEGTNCIDVDECLRPDVCGBGHCVNTVGAFRCEYCDSGYR 662
Qy      119  MDESNOQCVDDDECATDSHQCNPTQICINTEGGYTC-SCTDGYWLLLEGQCLDIDEC-RYGY 176
Db      663  MTQRGRCEDIDECCLNPS-TC-PDBQCVNSPFGSYQCVPTCEGFRGMNGQCLDVEDECLEPNV 720
Qy      177  CQQ-LCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQ----- 219
Db      721  CANGDCSNLBSYMCSCCHKGYTRTPDHKHCARDIDECQQGNLCVNGQCKNTEGSFRCTCGQ 780
Qy      220  -----TCVNTYGSFICRCDPGYELEEDGVHCSMDMECSF 253
Db      781  GYQLSAAKDQCEDIDECQHRHLCAHGQCRNTEGSPQCVCQGYRASGLGDHCEDINECLE 840
Qy      254  SEFLQQH-ECVNPQGYTYPCSCPPGYILLDDNRSQDINECEHRNHTCNLQQTICYNLQGGF 312
Db      841  DKSVCQRGDCINTAGSYDCTCPDGF-QLDDNKTCQDINECEHPG-LCGPQGECLNTEGSF 898
Qy      313  KCI-----DPIRCEEPYLRI-----DN-----RCMC-----PAENPGCR 342
Db      899  HCVQQQGFISADGRTCEDIDECVNNIVCDSHGFCNTAGSFRLCYQGFQAPQDGGQCV 958
Qy      343  DQPFTILYRDMDVVSG 358
Db      959  D-----VNECELLSG 968

```

# RESULT 14

```

US-09-482-273-159
; Sequence 159, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: PZ030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 159
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-482-273-159

```

Query Match 20.6%; Score 521.5; DB 4; Length 575;  
 Best Local Similarity 29.4%; Pred. No. 1.2e-33;  
 Matches 144; Conservative 58; Mismatches 164; Indels 123; Gaps 21;

```

Qy      13 LALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRT 72
      || : : : | ||:| | | :|:| | | || | | | | |
Db      157 LATALQAEEN-EVGCPEGFELDSQGAFCVDVDECAWAHLCREGRQCVNLLGSYRCLPDC 215

Qy      73 NPVYRGYPYSPYSTPYSGPYFAAAPPLSAFNYPTISRPLICRFQYQMDENQCVDVDECA 132
      | | | | | | | | | | | | | | | | | | | | |
Db      216 GP-----GFRVADGAGCEDVDECL 234

Qy      133 TDSHCNPTQICINTEGGYTCSCTDGYWLLEG---QCLDIDECRY--GYCQQLCANVPGS 187
      | : | : | | | : | | | | : | | | | | | | | |
Db      235 EGLDDCHYNQLCENTPGGHRCSFCRGY-RMQGPSLPCLDVNECLQLPKACAYQCHNLQGS 293

Qy      188 YSCNCPGFTLNEDGRSC-----QDVNECATENPCV-----QTCVNTYGSFI---- 229
      | | | | | | | | | | | | | | | | | | | | |
Db      294 YRCLCPPGQTLRLDGKACTSLERNQNVTTVSHRGPLPLWLRPWASIPGTSYHAWVSLRP 353

Qy      230 -----CRCDPGYELEDGVHCSMDDECSFSEFLCQHECVNPQGTYPFSCFPYGIL 279
      | | : : : | | : | | | | | | | | | | | | |
Db      354 GPMALSSVGRAMCPCPGF-IRQNGV-CTDLDECRVRN-LCQHACRNTEGSYQCLCPAGYRL 410

Qy      280 LDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCBEPYLRISDNRCMCPA--- 336
      | : | | | | | | : | | | | : | : | : | | |
Db      411 LPSPGKNQDINECEBESIECGPGQMCFNTRGSYQCVD-----TPCPATYR 455

Qy      337 --ENPG----CRDQ----PFTILYRDMDVVSGRSVPADIFQMATT--YPGAYYIFQ 382
      | | | | | | | | | | | | | | | | | | | | |
Db      456 QGPSFGTCFRRCSDCGTGGPSTLQYRLPLPLGVRAHHDVARLTAFSEVGVFANRTELS 515

Qy      383 IKSQNEGREFYMRQTGPISATL--VMTRPIKGPRI-QLDLEMITVNTVINFRGSSVIRL 439
      : : : | : | : | | | | | : : | : | | | |
Db      516 MLEPDRPSFPALR---PLRAGLGAVYTR----RALTRAGLYRLTVRAAP-RHQSVFVL 566

Qy      440 RIYVSQYPF 448
      | | | | :
Db      567 LIAVSPYPY 575
  
```

# RESULT 15

US-09-482-273-245  
 ; Sequence 245, Application US/09482273  
 ; Patent No. 6534631  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 71 Human Secreted Proteins  
 ; FILE REFERENCE: P2030P1  
 ; CURRENT APPLICATION NUMBER: US/09/482,273  
 ; CURRENT FILING DATE: 2000-01-13  
 ; EARLIER APPLICATION NUMBER: PCT/US99/15849  
 ; EARLIER FILING DATE: 1999-07-14  
 ; EARLIER APPLICATION NUMBER: 60/092,921  
 ; EARLIER FILING DATE: 1998-07-15  
 ; EARLIER APPLICATION NUMBER: 60/092,922



; EARLIER FILING DATE: 1998-07-15  
 ; EARLIER APPLICATION NUMBER: 60/092,956  
 ; EARLIER FILING DATE: 1998-07-15  
 ; NUMBER OF SEQ ID NOS: 267  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 245  
 ; LENGTH: 638  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-482-273-245

Query Match 20.6%; Score 521.5; DB 4; Length 638;  
 Best Local Similarity 29.4%; Pred. No. 1.4e-33;  
 Matches 144; Conservative 58; Mismatches 164; Indels 123; Gaps 21;

```

Qy      13 LALCLFSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRT 72
      || | : | : | ||: || | : || || | | | | | |
Db      220 LATALQAEEN-EVGCPEGFELDSQGAFCVDVDECAWDAHLCREGQRCVNLLGSGYRCLFDC 278

Qy      73 NPVYRGYPNSPYSTPYSPGYPA AAPLSAPNYPTISRPLICRFQYQMDENQCVDVDECA 132
      | | | | | | | | | | | | | | | | | | | | | |
Db      279 GP-----GFRVADGAGCEDVDECL 297

Qy      133 TDSHCNPTQICINTEGGYTCSCTIDGYWLLG---QCLDIDECRY--GYCQQLCANVPGS 187
      | : | : | | | | | | | | | | | | | | | |
Db      298 EGLDDCHYNQLCENTPGGHRCS CPRGY-RMQGPSLPCLDVNECLQLPKACAYQCHNLQGS 356

Qy      188 YSCTCNPGFTLNEDGRSC-----QDVNECATENPCV-----QTCVNTYGSFI---- 229
      | | | | | | | | | | | | | | | | | | | | | |
Db      357 YRCLCPPGQTLLRDGKACTSLERNQNVTTVSHRGPLLPWLRPWASIPGTSYHAWVSLRP 416

Qy      230 -----CRCDPGYELEDGVHCSMDDECSFSEFLCQHECVNPGFTYFCSCPPGYIL 279
      | | | : : | | | : | | | | | | | | | | | |
Db      417 GPMALSSVGRACPPGF-IRQNGV-CTDLDECRVRN-LCQHACRNTEGSYQCLCPAGYRL 473

Qy      280 LDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEBPYLRISDNRCMCPA--- 336
      | : | | | | | | : | | | : | : | : | | | |
Db      474 LPSGKNQDINECEESIECGPGQMCFNTRGSYQVD-----TPCPATYR 518

Qy      337 --ENPG----CRDQ-----PFTILYRDMDVVSGRSVPADIFQMATT--YPGAYYIFQ 382
      : | | | | | | | | | | | | | | | | | |
Db      519 QGPSFGTCFRRCSSQDCGTGGPSTLQYRLPLPLGVRAHHDVARLTAFSEVGVPANRTELS 578

Qy      383 IKSGNEGREFPYMRQTGPISATL--VMTRPIKGPRI-QLDLEMITVNTVINFRGSSVIRL 439
      : : | | | | | | | | | | | | | | | |
Db      579 MLEDPDRSPFALR---PLRAGLGAVYTR---RALTRAGLYRLTVRAAP-RHQSVFVL 629

Qy      440 RIYVSQYPF 448
      | | | |
Db      630 LIAVSPYPY 638
  
```

Search completed: January 9, 2004, 12:35:35  
 Job time : 17.9449 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2004, 12:34:12 ; Search time 29.8324 Seconds  
(without alignments)  
3026.121 Million cell updates/sec

Title: US-09-674-379A-13  
Perfect score: 2533  
Sequence: 1 MPGIKRLITVTILALCLPSP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match Length DB ID					Description

1	2533	100.0	448	9	US-09-083-002-2	Sequence 2, Appli
2	2533	100.0	448	9	US-09-275-805-2	Sequence 2, Appli
3	2533	100.0	448	9	US-09-836-561-1	Sequence 1, Appli
4	2533	100.0	448	14	US-10-041-016-2	Sequence 2, Appli
5	2527	99.8	448	12	US-10-199-672-408	Sequence 408, App
6	2527	99.8	448	12	US-10-187-749-408	Sequence 408, App
7	2527	99.8	448	12	US-10-194-457-408	Sequence 408, App
8	2527	99.8	448	12	US-10-184-642-408	Sequence 408, App
9	2527	99.8	448	12	US-10-196-747-408	Sequence 408, App
10	2527	99.8	448	12	US-10-173-689-408	Sequence 408, App
11	2527	99.8	448	12	US-10-173-690-408	Sequence 408, App
12	2527	99.8	448	12	US-10-173-691-408	Sequence 408, App
13	2527	99.8	448	12	US-10-173-692-408	Sequence 408, App
14	2527	99.8	448	12	US-10-173-694-408	Sequence 408, App
15	2527	99.8	448	12	US-10-173-698-408	Sequence 408, App
16	2527	99.8	448	12	US-10-173-699-408	Sequence 408, App
17	2527	99.8	448	12	US-10-173-707-408	Sequence 408, App
18	2527	99.8	448	12	US-10-174-569-408	Sequence 408, App
19	2527	99.8	448	12	US-10-174-583-408	Sequence 408, App
20	2527	99.8	448	12	US-10-174-587-408	Sequence 408, App
21	2527	99.8	448	12	US-10-174-589-408	Sequence 408, App
22	2527	99.8	448	12	US-10-174-591-408	Sequence 408, App
23	2527	99.8	448	12	US-10-175-736-408	Sequence 408, App
24	2527	99.8	448	12	US-10-175-742-408	Sequence 408, App
25	2527	99.8	448	12	US-10-175-744-408	Sequence 408, App
26	2527	99.8	448	12	US-10-175-745-408	Sequence 408, App
27	2527	99.8	448	12	US-10-175-748-408	Sequence 408, App
28	2527	99.8	448	12	US-10-175-751-408	Sequence 408, App
29	2527	99.8	448	12	US-10-175-754-408	Sequence 408, App
30	2527	99.8	448	12	US-10-176-480-408	Sequence 408, App
31	2527	99.8	448	12	US-10-176-489-408	Sequence 408, App
32	2527	99.8	448	12	US-10-176-754-408	Sequence 408, App
33	2527	99.8	448	12	US-10-176-755-408	Sequence 408, App
34	2527	99.8	448	12	US-10-176-759-408	Sequence 408, App
35	2527	99.8	448	12	US-10-176-920-408	Sequence 408, App
36	2527	99.8	448	12	US-10-176-922-408	Sequence 408, App
37	2527	99.8	448	12	US-10-176-924-408	Sequence 408, App
38	2527	99.8	448	12	US-10-176-984-408	Sequence 408, App
39	2527	99.8	448	12	US-10-179-508-408	Sequence 408, App
40	2527	99.8	448	12	US-10-179-512-408	Sequence 408, App
41	2527	99.8	448	12	US-10-179-515-408	Sequence 408, App
42	2527	99.8	448	12	US-10-066-198-15	Sequence 15, Appl
43	2527	99.8	448	12	US-10-173-702-408	Sequence 408, App
44	2527	99.8	448	12	US-10-173-703-408	Sequence 408, App
45	2527	99.8	448	12	US-10-173-704-408	Sequence 408, App

# ALIGNMENTS

RESULT 1  
 US-09-083-002-2  
 ; Sequence 2, Application US/09083002  
 ; Patent No. US20010016650A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jacobs, Kenneth

; APPLICANT: McCoy, John M.  
 ; APPLICANT: Racie, Lisa A.  
 ; APPLICANT: LaVallie, Edward R.  
 ; APPLICANT: Merberg, David  
 ; APPLICANT: Treacy, Maurice  
 ; APPLICANT: Evans, Cheryl  
 ; APPLICANT: Agostino, Michael  
 ; APPLICANT: Lu, Zhijian  
 ; APPLICANT: Honjo, Tasuku  
 ; APPLICANT: Tashiro, Kei  
 ; APPLICANT: Nakamura, Tomoyuki  
 ; TITLE OF INVENTION: SECRETED PROTEINS  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genetics Institute, Inc.  
 ; STREET: 87 CambridgePark Drive  
 ; CITY: Cambridge  
 ; STATE: MA  
 ; COUNTRY: U.S.A.  
 ; ZIP: 02140  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/083,002  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sprunger, Suzanne A.  
 ; REGISTRATION NUMBER: P-41,323  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 498-8284  
 ; TELEFAX: (617) 876-5851  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 448 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: not relevant  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-09-083-002-2

Query Match 100.0%; Score 2533; DB 9; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-192;  
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPGIKRIILTVTILALCLSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MPGIKRIILTVTILALCLSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60  
 Qy 61 NQNGGYLCIPRTNPFVIRGYPYSNFYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 NQNGGYLCIPRTNPFVIRGYPYSNFYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120  
 Qy 121 ESNQCVDVDECATDSHCNPTQICINTEGGYTCSDTGDYWLLEGQCLDIDECRYGYCQQL 180

Db 121 |||||ESNQCVVDSCATDSHQCNPTQICINTEGGYTCSCDTGYWLLLEGQCLDIDBCRYGYCQQL 180  
 Qy 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
 Db 181 |||||CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
 Qy 241 DGVHCSMDMECSFSFELCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300  
 Db 241 |||||DGVHCSMDMECSFSFELCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300  
 Qy 301 LQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPTTILYRDMDVVSGRS 360  
 Db 301 |||||LQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPTTILYRDMDVVSGRS 360  
 Qy 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420  
 Db 361 |||||VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420  
 Qy 421 EMITVNTVINFRGSSVIRLRIYVSQYFF 448  
 Db 421 |||||EMITVNTVINFRGSSVIRLRIYVSQYFF 448

# RESULT 2

US-09-275-805-2

; Sequence 2, Application US/09275805

; Patent No. US20010051358A1

; GENERAL INFORMATION:

; APPLICANT: OLSEN, HENRIK S.

; APPLICANT: LI, HAODONG

; TITLE OF INVENTION: EXTRACELLULAR EPIDERMAL GROWTH FACTOR

; TITLE OF INVENTION: LIKE PROTEIN

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVENUE

; CITY: ROCKVILLE

; STATE: MD

; COUNTRY: US

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/275,805

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/839,525

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: BROOKES, ANDERS A.

; REGISTRATION NUMBER: 36,373

; REFERENCE/DOCKET NUMBER: PF224

; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (301) 309-8509  
 ; TELEFAX: (301) 309-8512  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 448 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-09-275-805-2

Query Match 100.0%; Score 2533; DB 9; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-192;  
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSQCLDIDECRTIPEACRGDMMCV 60
      |||
Db      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSQCLDIDECRTIPEACRGDMMCV 60

QY     61  NQNGGYLCIPRTNPVIRGYPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
      |||
Db     61  NQNGGYLCIPRTNPVIRGYPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

QY    121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQL 180
      |||
Db    121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQL 180

QY    181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYBLEE 240
      |||
Db    181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYBLEE 240

QY    241  DGVHCSMDDECSFSEFLCQHECVNQPQTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300
      |||
Db    241  DGVHCSMDDECSFSEFLCQHECVNQPQTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300

QY    301  LQQTTCYNLQGGFKCIDPIRCEEPYLRI SDNRCMC PAENPGCRDQPFTILYRDM DVVSGRS 360
      |||
Db    301  LQQTTCYNLQGGFKCIDPIRCEEPYLRI SDNRCMC PAENPGCRDQPFTILYRDM DVVSGRS 360

QY    361  VPADIFQM QATTTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMT RPIKGP REIQLDL 420
      |||
Db    361  VPADIFQM QATTTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMT RPIKGP REIQLDL 420

QY    421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
      |||
Db    421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
  
```

RESULT 3

US-09-836-561-1

; Sequence 1, Application US/09836561

; Patent No. US20020038006A1

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; Corley, Neil C.

; Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/836,561  
 ; FILING DATE: 16-Apr-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/212,168  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PP-0333 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-855-0555  
 ; TELEFAX: 415-845-4166  
 ; TELEX: <Unknown>  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 448 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: CORNNOT01  
 ; CLONE: 45517  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-836-561-1

Query Match 100.0%; Score 2533; DB 9; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-192;  
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1  MPGIKRILTVTILALCLSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
         |||||||
Db      1  MPGIKRILTVTILALCLSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61  NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYAAAPLSAPNYPTISRPLICRFGYQMD 120
         |||||||
Db     61  NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYAAAPLSAPNYPTISRPLICRFGYQMD 120

Qy    121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSTCDGYWLLLEGQCLDIDECRYGYCQQL 180
         |||||||
Db    121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSTCDGYWLLLEGQCLDIDECRYGYCQQL 180

Qy    181  CANVPGSYSSTCNPGFTLNEGDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
  
```

Db 181 |||||CANVPGSYSTCMPTFLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELE 240  
 QY 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300  
 Db 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300  
 QY 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRIISDNRCMCPAENPGCRDQPTILYRDMOVVSGRS 360  
 Db 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRIISDNRCMCPAENPGCRDQPTILYRDMOVVSGRS 360  
 QY 361 VPADIFQMQATTTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420  
 Db 361 VPADIFQMQATTTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420  
 QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448  
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 4

US-10-041-016-2

; Sequence 2, Application US/10041016

; Publication No. US20020165151A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth  
 ; McCoy, John M.  
 ; Racie, Lisa A.  
 ; LaVallie, Edward R.  
 ; Merberg, David  
 ; Treacy, Maurice  
 ; Evans, Cheryl  
 ; Agostino, Michael  
 ; Lu, Zhijian  
 ; Honjo, Tasuku

; TITLE OF INVENTION: SECRETED PROTEINS

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.  
 ; STREET: 87 CambridgePark Drive  
 ; CITY: Cambridge  
 ; STATE: MA  
 ; COUNTRY: U.S.A.  
 ; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/041,016  
 ; FILING DATE: 07-Jan-2002  
 ; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/083,002  
 ; FILING DATE: 21-MAR-1998

; ATTORNEY/AGENT INFORMATION:



```

;      NAME: Sprunger, Suzanne A.
;      REGISTRATION NUMBER: P-41,323
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (617) 498-8284
;      TELEFAX: (617) 876-5851
;      INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 448 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: No. US20020165151A1 Relevant
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-041-016-2

```

```

Query Match      100.0%; Score 2533; DB 14; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.9e-192;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQLDIDECRTIPEACRGDMMCV 60
      |||
Db      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQLDIDECRTIPEACRGDMMCV 60

Qy      61  NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
      |||
Db      61  NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy      121  ESNQCVVDVDECATDSHQCNPTQICINTEGGYTCSDTGYNLLEGGQLDIDECRYGYCQQL 180
      |||
Db      121  ESNQCVVDVDECATDSHQCNPTQICINTEGGYTCSDTGYNLLEGGQLDIDECRYGYCQQL 180

Qy      181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
      |||
Db      181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy      241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300
      |||
Db      241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300

Qy      301  LQQTTCYNLQGGFKCIDPIRCEEPYLRLISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360
      |||
Db      301  LQQTTCYNLQGGFKCIDPIRCEEPYLRLISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360

Qy      361  VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTREIKGPREIQLDL 420
      |||
Db      361  VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTREIKGPREIQLDL 420

Qy      421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
      |||
Db      421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448

```

# RESULT 5

US-10-199-672-408

; Sequence 408, Application US/10199672

; Publication No. US20030148442A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3430R1C1  
 ; CURRENT APPLICATION NUMBER: US/10/199,672  
 ; CURRENT FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: US/10/052,586  
 ; PRIOR FILING DATE: 2002-01-15  
 ; PRIOR APPLICATION NUMBER: 60/059263  
 ; PRIOR FILING DATE: 1997-09-18  
 ; PRIOR APPLICATION NUMBER: 60/059266  
 ; PRIOR FILING DATE: 1997-09-18  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063120  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/063121  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/063486  
 ; PRIOR FILING DATE: 1997-10-21  
 ; PRIOR APPLICATION NUMBER: 60/063540  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/063541  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/063544  
 ; PRIOR FILING DATE: 1997-10-28  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 408  
 ; LENGTH: 448  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-199-672-408

Query Match 99.8%; Score 2527; DB 12; Length 448;  
 Best Local Similarity 99.8%; Pred. No. 5.7e-192;  
 Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1  MPGIKRILTVTILALCLSPGNAQAQCTNGFDLDRQSGQLDIDECRTIPEACRGDMMCV 60
      |||
Db      1  MPGIKRILTVTILALCLSPGNAQAQCTNGFDLDRQSGQLDIDECRTIPEACRGDMMCV 60
      |||

Qy      61  NQNGGYLCIPRTNPVYRGFYSNPFYSTPYSGPYAAAPLSAPNYPPTISRPLICRFGYQMD 120
      |||
Db      61  NQNGGYLCIPRTNPVYRGFYSNPFYSTPYSGPYAAAPLSAPNYPPTISRPLICRFGYQMD 120
      |||

Qy      121  ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQL 180
```

Db	121		180
Qy	181		240
Db	181		240
Qy	241		300
Db	241		300
Qy	301		360
Db	301		360
Qy	361		420
Db	361		420
Qy	421		448
Db	421		448

RESULT 6

US-10-187-749-408

; Sequence 408, Application US/10187749

; Publication No. US20030153036A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C1

; CURRENT APPLICATION NUMBER: US/10/187,749

; CURRENT FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: US/10/052,586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486  
 ; PRIOR FILING DATE: 1997-10-21  
 ; PRIOR APPLICATION NUMBER: 60/063540  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/063541  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/063544  
 ; PRIOR FILING DATE: 1997-10-28  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 408  
 ; LENGTH: 448  
 ; TYPE: PRF  
 ; ORGANISM: Homo Sapien  
 US-10-187-749-408

Query Match 99.8%; Score 2527; DB 12; Length 448;  
 Best Local Similarity 99.8%; Pred. No. 5.7e-192;  
 Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy      1  MPGIKRILFTVITLALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MPGIKRILFTVITLALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61  NQNGGYLCIPRTNPFVYRGYPYSNPFYSTPYSGGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  NQNGGYLCIPRTNPFVYRGYPYSNPFYSTPYSGGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy    121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQL 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQL 180

Qy    181  CANVPGSYSCNCPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CANVPGSYSCNCPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy    241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

Qy    301  LQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRDQPFITILYRDMDVVSGRS 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  LQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRDQPFITILYRDMDVVSGRS 360

Qy    361  VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420

Qy    421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
      ||||||||||||||||||||||||||||
Db    421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
  
```

RESULT 7  
 US-10-194-457-408  
 ; Sequence 408, Application US/10194457  
 ; Publication No. US20030153037A1

```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C296
; CURRENT APPLICATION NUMBER: US/10/194,457
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-457-408

```

```

Query Match          99.8%; Score 2527; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 5.7e-192;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 MPGIKRILTVTILALCLSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
        |||
Db      1 MPGIKRILTVTILALCLSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
        |||

Qy      61 NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD 120
        |||
Db      61 NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD 120
        |||

```

Qy 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCCTDGYWLLGGQCLDIDECYRGYCOQL 180  
 |||||  
 Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCCTDGYWLLGGQCLDIDECYRGYCOQL 180  
 |||||  
 Qy 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYEELE 240  
 |||||  
 Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYEELE 240  
 |||||  
 Qy 241 DGVHCSMDMECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |||||  
 Db 241 DGVHCSMDMECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |||||  
 Qy 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMOVVSGRS 360  
 |||||  
 Db 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMOVVSGRS 360  
 |||||  
 Qy 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420  
 |||||  
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420  
 |||||  
 Qy 421 EMITVNTVINFRGSSVIRLRIYVSQYFF 448  
 |||||  
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYFF 448  
 |||||

RESULT 8

US-10-184-642-408

; Sequence 408, Application US/10184642

; Publication No. US20030157635A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C194

; CURRENT APPLICATION NUMBER: US/10/184,642

; CURRENT FILING DATE: 2002-06-27

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-184-642-408

Query Match 99.8%; Score 2527; DB 12; Length 448;

Best Local Similarity 99.8%; Pred. No. 5.7e-192;

Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPGIKRILTVTILALCLPSGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60  
 |||||  
 Db 1 MPGIKRILTVTILALCLPSGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60  
 |||||  
 Qy 61 NQNGGYLCIPRTNPVYRGFYSNPFYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120  
 |||||  
 Db 61 NQNGGYLCIPRTNPVYRGFYSNPFYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120  
 |||||  
 Qy 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQL 180  
 |||||  
 Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQL 180  
 |||||  
 Qy 181 CANVPGSYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
 |||||  
 Db 181 CANVPGSYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
 |||||  
 Qy 241 DGVHCSMDMECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |||||  
 Db 241 DGVHCSMDMECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |||||  
 Qy 301 LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITLYRDMDVVSGRS 360  
 |||||  
 Db 301 LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITLYRDMDVVSGRS 360  
 |||||  
 Qy 361 VPADIFQMQAATTYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420  
 |||||  
 Db 361 VPADIFQMQAATTYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420  
 |||||  
 Qy 421 EMITVNTVINFRGSSVIRLRIYVSQYFF 448  
 |||||  
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYFF 448  
 |||||

RESULT 9

US-10-196-747-408

; Sequence 408, Application US/10196747

; Publication No. US20030162250A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C346

; CURRENT APPLICATION NUMBER: US/10/196,747

; CURRENT FILING DATE: 2002-07-16

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-196-747-408

Query Match 99.8%; Score 2527; DB 12; Length 448;  
Best Local Similarity 99.8%; Pred. No. 5.7e-192;  
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
      |||
Db      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61  NQNGGYLCIPRTNPVYRGPYSNFYSTPYSGPYAAAPLSAPNYPTISRPLICRFGYQMD 120
      |||
Db     61  NQNGGYLCIPRTNPVYRGPYSNFYSTPYSGPYAAAPLSAPNYPTISRPLICRFGYQMD 120

Qy    121  ESNQCVDVDECATDSHCNPTQICINTEGGYTCSTDGYWLLBGQCLDIDECRYGYCQQL 180
      |||
Db    121  ESNQCVDVDECATDSHCNPTQICINTEGGYTCSTDGYWLLBGQCLDIDECRYGYCQQL 180

Qy    181  CANVPGSYSCTCNPGFTLNEGDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
      |||
Db    181  CANVPGSYSCTCNPGFTLNEGDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy    241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQCDINECEHRNHTCN 300
      |||
Db    241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQCDINECEHRNHTCN 300

Qy    301  LQQTCTYNLQGGFKCIDPIRCEEPYLRIISDNRCMCPAENPGCRDQPFTILYRMDVVSGRS 360
      |||
Db    301  LQQTCTYNLQGGFKCIDPIRCEEPYLRIISDNRCMCPAENPGCRDQPFTILYRMDVVSGRS 360

Qy    361  VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPKIGPREIQLDL 420
      |||
Db    361  VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPKIGPREIQLDL 420

Qy    421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
      |||
Db    421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
```

RESULT 10

US-10-173-689-408

; Sequence 408, Application US/10173689

; Publication No. US20030166104A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.



; APPLICANT: Wood,William I.  
 ; APPLICANT: Zhang,Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3430R1C10  
 ; CURRENT APPLICATION NUMBER: US/10/173,689  
 ; CURRENT FILING DATE: 2002-06-17  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 408  
 ; LENGTH: 448  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-173-689-408

Query Match 99.8%; Score 2527; DB 12; Length 448;  
 Best Local Similarity 99.8%; Pred. No. 5.7e-192;  
 Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
      |||
Db      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61  NQNGGYLCIPRTNPFVYRGFYSNPYSTFPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD 120
      |||
Db     61  NQNGGYLCIPRTNPFVYRGFYSNPYSTFPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy     121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSDTGYWLLLEGQCLDIDECRYGYCQQL 180
      |||
Db     121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSDTGYWLLLEGQCLDIDECRYGYCQQL 180

Qy     181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
      |||
Db     181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy     241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYIILLDDNRSQDINECEHRNHTCN 300
      |||
Db     241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYIILLDDNRSQDINECEHRNHTCN 300

Qy     301  LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360
      |||
Db     301  LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360

Qy     361  VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPICKGPREIQLDL 420
      |||
Db     361  VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPICKGPREIQLDL 420

Qy     421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
      |||
Db     421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
  
```

# RESULT 11

US-10-173-690-408  
 ; Sequence 408, Application US/10173690  
 ; Publication No. US20030166105A1  
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3430R1C9  
 ; CURRENT APPLICATION NUMBER: US/10/173,690  
 ; CURRENT FILING DATE: 2002-06-17  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 408  
 ; LENGTH: 448  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-173-690-408

Query Match 99.8%; Score 2527; DB 12; Length 448;  
 Best Local Similarity 99.8%; Pred. No. 5.7e-192;  
 Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
      |||
Db      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy      61  NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD 120
      |||
Db      61  NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy      121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLBQGLDIDECRYGYCQQL 180
      |||
Db      121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLBQGLDIDECRYGYCQQL 180

Qy      181  CANVPGSYSCTCNPGFITLNEGRSCQDVNECATENPCVQTCVNTYGSPIRCDDPGYELEE 240
      |||
Db      181  CANVPGSYSCTCNPGFITLNEGRSCQDVNECATENPCVQTCVNTYGSPLICRCDPGYELEE 240

Qy      241  DGVHCSMDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300
      |||
Db      241  DGVHCSMDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN 300

Qy      301  LQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPPTILYRDMDVVSGRS 360
      |||
Db      301  LQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPPTILYRDMDVVSGRS 360

Qy      361  VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
      |||
Db      361  VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420

Qy      421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
  
```

Db

|||||  
421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

## RESULT 12

US-10-173-691-408

; Sequence 408, Application US/10173691

; Publication No. US20030166106A1

## ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C13

; CURRENT APPLICATION NUMBER: US/10/173,691

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408

; LENGTH: 448

; TYPE: PRF

; ORGANISM: Homo Sapien

US-10-173-691-408

Query Match 99.8%; Score 2527; DB 12; Length 448;

Best Local Similarity 99.8%; Pred. No. 5.7e-192;

Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy      1  MPGIKRILTVTILALCLPSGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
      |||
Db      1  MPGIKRILTVTILALCLPSGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy      61  NQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
      |||
Db      61  NQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy      121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQL 180
      |||
Db      121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQL 180

Qy      181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
      |||
Db      181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy      241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
      |||
Db      241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

```



Qy 181 CANVFGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240  
 |||  
 Db 181 CANVFGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFLICRCDPGYELEE 240  
 |||  
 Qy 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |||  
 Db 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |||  
 Qy 301 LQOTCYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS 360  
 |||  
 Db 301 LQOTCYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS 360  
 |||  
 Qy 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420  
 |||  
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420  
 |||  
 Qy 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448  
 |||  
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448  
 |||

# RESULT 14

US-10-173-694-408

; Sequence 408, Application US/10173694

; Publication No. US20030166107A1

## ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C19

; CURRENT APPLICATION NUMBER: US/10/173,694

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-173-694-408

Query Match 99.8%; Score 2527; DB 12; Length 448;

Best Local Similarity 99.8%; Pred. No. 5.7e-192;

Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLRQSGCQLDIDECRTIPEACRGDMCMV 60  
 |||

Db 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTYPEACRGDMMCV 60

QY 61 NQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120  
 |||

Db 61 NQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120  
 |||

QY 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCDTGYNLLEGGQCLDIDECYGYCQQL 180  
 |||

Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCDTGYNLLEGGQCLDIDECYGYCQQL 180  
 |||

QY 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSPICRCDPGYELEB 240  
 |||

Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSPICRCDPGYELEB 240  
 |||

QY 241 DGVHCSMDDECSFSEFLQHECVNQPPTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |||

Db 241 DGVHCSMDDECSFSEFLQHECVNQPPTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300  
 |||

QY 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMVVSGRS 360  
 |||

Db 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMVVSGRS 360  
 |||

QY 361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRIKGPRIQLDL 420  
 |||

Db 361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRIKGPRIQLDL 420  
 |||

QY 421 EMITVNTVINFRGSSVIRLRIYVSQYFF 448  
 |||

Db 421 EMITVNTVINFRGSSVIRLRIYVSQYFF 448  
 |||

RESULT 15

US-10-173-698-408

; Sequence 408, Application US/10173698

; Publication No. US20030166108A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C12

; CURRENT APPLICATION NUMBER: US/10/173,698

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo Sapien  
US-10-173-698-408

Query Match 99.8%; Score 2527; DB 12; Length 448;  
Best Local Similarity 99.8%; Pred. No. 5.7e-192;  
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1  MPGIKRIILTITLALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MPGIKRIILTITLALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61  NQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  NQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy    121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQL 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQL 180

Qy    181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDFGYELE 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDFGYELE 240

Qy    241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

Qy    301  LQQTCTYNLQGGPKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  LQQTCTYNLQGGPKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360

Qy    361  VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPKGPREIQDL 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPKGPREIQDL 420

Qy     421  EMITVNTVINFRGSSVIRLRIYVSQYFF 448
      ||||||||||||||||||||||||||||
Db     421  EMITVNTVINFRGSSVIRLRIYVSQYFF 448
```

Search completed: January 9, 2004, 12:43:58  
Job time : 30.8324 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2004, 12:29:16 ; Search time 16.9736 Seconds  
(without alignments)  
2538.270 Million cell updates/sec

Title: US-09-674-379A-13  
Perfect score: 2533  
Sequence: 1 MPGIKRLTVTILALCLPSP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1109.5	43.8	493	2	JC5621	epidermal growth f
2	963.5	38.0	387	2	I38449	extracellular prot
3	746	29.5	685	2	S78040	fibulin, splice fo
4	737	29.1	683	2	C36346	fibulin 1 precurs
5	733.5	29.0	1221	2	A49457	fibulin-2 precurs
6	709.5	28.0	1184	2	A55184	fibulin-2 precurs
7	703.5	27.8	705	2	S34968	fibulin, splice fo
8	619	24.4	601	2	B36346	fibulin 1 precurs
9	606.5	23.9	689	2	T42760	fibulin, splice fo
10	599.5	23.7	712	2	T42990	fibulin 1, splice
11	596	23.5	589	2	T43210	fibulin-1D precurs
12	577.5	22.8	798	2	T22793	hypothetical prote
13	544	21.5	1394	2	A35626	transforming growt



14	532.5	21.0	3002	2	A47221	fibrillin 1 precur
15	531.5	21.0	2871	2	A55567	fibrillin I - bovi
16	523	20.6	1712	2	A38261	masking protein pr
17	518.5	20.5	2871	2	A55624	fibrillin-1 precur
18	518.5	20.5	2907	2	A57278	fibrillin-2 precur
19	517.5	20.4	2918	2	A54105	fibrillin-2 precur
20	480.5	19.0	1820	2	A55494	latent transformin
21	475	18.8	741	2	T46488	hypothetical prote
22	461	18.2	1251	2	A57293	latent transformin
23	459	18.1	1620	2	T27283	hypothetical prote
24	444	17.5	1574	2	T13954	MEGF6 protein - ra
25	392	15.5	886	2	A57172	probable hormone r
26	388	15.3	3507	2	T34513	hypothetical prote
27	372.5	14.7	1106	2	T18739	hypothetical prote
28	371.5	14.7	2471	2	A49128	cell-fate determin
29	365.5	14.4	1203	2	A49175	Notch B protein -
30	364	14.4	810	2	T10756	Nel-homolog protei
31	361	14.3	1081	2	T31329	receptor tyrosine
32	359.5	14.2	1964	2	T09059	notch4 - mouse
33	359	14.2	511	2	T17298	hypothetical prote
34	358	14.1	2555	2	A40043	notch protein homo
35	356	14.1	2703	1	A24420	notch protein - fr
36	355.5	14.0	2437	2	S42612	transmembrane prot
37	346	13.7	1064	2	A40136	fibropellin Ia - s
38	346	13.7	2524	2	A35844	Xotch protein - Af
39	344	13.6	2321	2	S78549	notch3 protein - h
40	340.5	13.4	673	2	A48089	growth arrest-spec
41	337.5	13.3	2318	2	S45306	notch 3 protein -
42	337.5	13.3	2531	2	S18188	notch protein homo
43	337	13.3	2531	2	T31070	notch homolog - se
44	335.5	13.2	674	2	I55476	growth potentiati
45	335	13.2	2531	2	A46019	notch-1 protein -

#### ALIGNMENTS

##### RESULT 1

JC5621

epidermal growth factor-like protein, T16 precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1997 #sequence\_revision 07-Nov-1997 #text\_change 05-Nov-1999

C;Accession: JC5621

R;Ozaki, T.; Kondo, K.; Nakamura, Y.; Ichimiya, S.; Nakagawara, A.; Sakiyama, S. Biochem. Biophys. Res. Commun. 237, 245-250, 1997

A;Title: Interaction of DA41, a DAN-binding protein, with the epidermal growth factor-like protein, S(1-5).

A;Reference number: JC5621; MUID:97415782; PMID:9268694

A;Accession: JC5621

A;Molecule type: mRNA

A;Residues: 1-493 <OZA>

A;Cross-references: DDBJ:D89730; NID:g2429082; PIDN:BAA22265.1; PID:d1023127; PID:g2429083

C;Comment: This protein plays a role in the regulation of cell growth by interacting with DAN protein through DA41 protein.

C;Keywords: glycoprotein

F;1-17/Domain: signal sequence #status predicted <SIG>

F;28-70,158-199,200-237,238-277,278-318,319-359/Region: epidermal growth factor-like repeat

F;242/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 43.8%; Score 1109.5; DB 2; Length 493;  
Best Local Similarity 42.3%; Pred. No. 1.5e-65;  
Matches 206; Conservative 73; Mismatches 161; Indels 47; Gaps 5;

```
Qy      7 ILTVTILALCLPSGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGY 66
      :||: :: : |||:|:: | || |||| :|:|:| ||| |||
Db      9 MLTLALVKSQVTEETITTYTQCTDGYEWDVPRQCKDIDECDIVPDACKGGMKCVNHYGGY 68

Qy     67 LCIPRTNPVYRGYPYSPYSTPYS-----GYPFAAAPPLSAP 102
      ||:|:| : || : ||:|:| :|:|:| ::|
Db     69 LCLPKTAQIIVNNEQPQQTFAABASSGAATGTIAARSMATSGVIFGGGFIASATAVAGP 128

Qy     103 NYPT-----ISRPLICRFGYQMDENQCVDVDECATDSHCQNPTQ 142
      | : : ||: | ||:|:| :|:|:| :|
Db     129 EVQTRGRNFFVIRRNPADPQRIPSNPSHRIQCAAGYEQSEHNVCQDIDECTSGTHNCRLDQ 188

Qy     143 ICINTEGGYTCSTDGYWLLBGQCLDIDECRY-GYCCQLCANVPGSYSCTCNPGFTLNED 201
      :||| :|:| || |||:| ||| |||:| |||:| :|
Db     189 VCTNLRGSPTCHCLPGYQKRGEQCVDIDECSSVPPYCHQGCNVNTPGSFYCQCNPGFQLAAN 248

Qy     202 GRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYEELEDGVHCSMDDECSFSEFLCQHE 261
      :| |||:| ||| |||:| |||:|:| |||:|:| |||:|:|
Db     249 NYTCVDINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCDIDECRTSSYLQCYQ 308

Qy     262 CVNPGPTGYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCNYLQGGFKCIDPIRCE 321
      |||:| :| ||| :|:| |||:| |||:| |||:| |||:|
Db     309 CVNEPGKFSCMCPQGYQVV-RSRTCQDINECETTNE-CREDEMCKWNYHGGFRCYPQNPOQ 366

Qy     322 EPLYLRISDNRCMCPAENPGCRDQPFITILYRDMVDVSGRSVPADIFQMQATTRYPGAYYIF 381
      :||: |||:| ||| ||| |||:| |||:| |||:| |||:|
Db     367 DPYVLTSENRCVCPVSNMTCRDVPQSIYKYMNIRSDRSVPDIFQIQATTIYANTINTP 426

Qy     382 QIKSGNEGREFYMRQTGPISATLVMTTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRI 441
      :||| |||:| |||:| |||:| |||:| |||:| |||:|
Db     427 RIKSGNENGFBYLRQTSVPVSAMLVLVKSLTGPREHIVGLEMLTVSSIGTFRTSSVLRLLT 486

Qy     442 YVSQYPP 448
      | :|
Db     487 IVGPFSF 493
```

#### RESULT 2

I38449

extracellular protein - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000

C;Accession: I38449

R;Lecka-Czernik, B.; Lumpkin, C.K.

Mol. Cell. Biol. 15, 120-128, 1995

A;Title: An overexpressed gene transcript in senescent and quiescent human fibroblasts encoding a novel protein in the epidermal growth factor-like repeat family stimulates DNA synthesis.

A;Reference number: I38449; MUID:95097983; PMID:7799918

A;Accession: I38449  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-387 <RES>  
 A;Cross-references: EMBL:U03877; NID:g458227; PIDN:AAA65590.1; PID:g458228  
 C;Genetics:  
 A;Gene: S1-5

Query Match 38.0%; Score 963.5; DB 2; Length 387;  
 Best Local Similarity 48.3%; Pred. No. 4.4e-56;  
 Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

```

Qy      96 APPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPTQICINTEGGYTCSC 155
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy      156 TDGYWLLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE 214
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSPYQCSPGQLAANNYTCVDINECDAS 155

Qy      215 NPCVQTCVNTYGSFICRCDPGYLEEDGVHCSMDBCSFSEFLCQHECVNQPGTYFCSCFP 274
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      156 NQCAQQCYNILGSFICQCNQGYELSSDRNLNCEDEIDECTSSYLQCQYQCVNEPGKFSCMCP 215

Qy      275 PGYILLDDNRSQDINECEHRNHTCNLQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMC 334
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      216 QGYQVW-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCPYPRNQDPYILTPENRCVC 273

Qy      335 PAENPGCRDPQPTILYRDMDDVSGRSPADIFQMQATTRYPGAYYIFQIKSGNENGREFYM 394
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      274 PVSNAMCRELPQSIYVYKMSIRSDRSVPDIFQIQATTIYANTINTFRIKSGNENGEBFYL 333

Qy      395 RQTGPISATLVMTPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      334 RQTSVPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFTRTSSVLRLLTIIVGPFPF 387
  
```

# RESULT 3

S78040

fibulin, splice form C precursor - mouse

N;Alternate names: basement-membrane protein BM-90

C;Species: Mus musculus (house mouse)

C;Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 02-Aug-2002

C;Accession: S78040; S78560; S36440

R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.

Eur. J. Biochem. 215, 733-740, 1993

A;Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent binding to other basement-membrane ligands.

A;Reference number: S34968; MUID:93358897; PMID:8354280

A;Accession: S78040

A;Molecule type: mRNA

A;Residues: 1-685 <PAN>

A;Cross-references: EMBL:X70854

R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.

submitted to the EMBL Data Library, January 1993

A;Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent binding to other basement membrane ligands.

A;Reference number: S36440  
 A;Accession: S78560  
 A;Molecule type: mRNA  
 A;Residues: 1-39,'P',41-685 <CHU>  
 A;Cross-references: EMBL:X70854  
 C;Genetics:  
 A;Introns: 568/3  
 C;Superfamily: fibulin-1; EGF homology  
 C;Keywords: alternative splicing; basement membrane; calcium binding; extracellular matrix; glycoprotein; plasma  
 F;1-29/Domain: signal sequence #status predicted <SIG>  
 F;30-685/Product: fibulin, splice form C #status predicted <MAT>  
 F;98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.5%; Score 746; DB 2; Length 685;  
 Best Local Similarity 36.3%; Pred. No. 1.3e-41;  
 Matches 161; Conservative 64; Mismatches 153; Indels 66; Gaps 17;

```

Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV 75
      | | : | | : | | | | : | | : | | |
Db      290 CRP-----KLQCKSGFIQD-ALGNCIDINECLSIAPCPVGQTCINTEGSSYTC----- 336

Qy      76 YRGPYSNPYSTPYSGPYAAAPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD 134
      : | | : | | : | | : | | : | | | | |
Db      337 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAFP 365

Qy      135 SHQCNPTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS 189
      : | | : | | : | | : | | : | | | | |
Db      366 AEPQCKGHHCLNSPGSPRCECKAGFYFDGISRTQVDINEQRYPGRLQGHKCENTPGSPH 425

Qy      190 CTCNPGFTLNEGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELBE-DGVHCSDM 248
      | : | | | : | | | | | : | | : | | | | |
Db      426 CSCSAGFRLSVDRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDI 484

Qy      249 DECSF--SEFLQCHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQT 305
      | | | : | : | | | | | | | | | | | |
Db      485 DECALPTGGHICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCINETC 544

Qy      306 YNLQGGFKCIDPIRCEEPYLRISDNRCM---CPAENPGCRDPFTILYRMDVVSGRSVP 362
      : | : | | : | | | | : | | | | | | |
Db      545 FNIQGSFRCLF-FECPENYRRSADTRCARLPC-HENQECRLPLRITTYHLSFPTNIQVP 602

Qy      363 ADIFQMQATTRYPGAYYIFQIKSGNEGREBFYMRQTPISATLVMTRPKIGPREIQLDLEM 422
      | : | : | | | | | | | : | | : | : | | |
Db      603 AVVFRMGPSAVPGDSMLAITAGNEEGFFTRKRVSHHSGVVALTKPIEPRDLLLTVM 662

Qy      423 --ITVNTVINFRGSSVIRLRIYVS 444
      | | : | | : | |
Db      663 DLYRHGTVSSP----VAKLFIFVS 682
  
```

RESULT 4  
 C36346

fibulin 1 precursor, splice form C - human

N;Alternate names: fibulin C

N;Contains: fibulin 1 splice form A; fibulin 1 splice form C

C;Species: Homo sapiens (man)

C;Date: 19-Apr-1991 #sequence\_revision 19-Apr-1991 #text\_change 02-Aug-2002  
 C;Accession: C36346; A36346; A32826  
 R;Argaves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.  
 J. Cell Biol. 111, 3155-3164, 1990  
 A;Title: Fibulin is an extracellular matrix and plasma glycoprotein with repeated domain structure.  
 A;Reference number: A36346; MUID:91100426; PMID:2269669  
 A;Accession: C36346  
 A;Molecule type: mRNA  
 A;Residues: 1-683 <AR>  
 A;Cross-references: GB:X53743; NID:g31418; PIDN:CAA37772.1; PID:g31419  
 A;Accession: A36346  
 A;Molecule type: mRNA  
 A;Residues: 1-566 <AR2>  
 A;Cross-references: GB:X53741; NID:g31414; PIDN:CAA37770.1; PID:g31415  
 R;Argaves, W.S.; Dickerson, K.; Burgess, W.H.; Ruoslahti, E.  
 Cell 58, 623-629, 1989  
 A;Title: Fibulin, a novel protein that interacts with the fibronectin receptor beta-subunit cytoplasmic domain.  
 A;Reference number: A32826; MUID:89354537; PMID:2527614  
 A;Accession: A32826  
 A;Molecule type: protein  
 A;Residues: 30-35,'SX',38-40,'SH',43-44 <AR3>  
 C;Genetics:  
 A;Gene: GDB:FBLN1; FBLN  
 A;Cross-references: GDB:278285; OMIM:135820  
 A;Map position: 22q13.3-22q13.3  
 C;Superfamily: fibulin-1; EGF homology  
 C;Keywords: alternative splicing; glycoprotein  
 F;1-29/Domain: signal sequence #status predicted <SIG>  
 F;30-683/Product: fibulin 1 splice form C #status predicted <MAT>  
 F;180-214/Domain: EGF homology <EGF>  
 F;485-523/Domain: EGF homology <EGF1>  
 F;98,535,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.1%; Score 737; DB 2; Length 683;  
 Best Local Similarity 35.4%; Pred. No. 4.9e-41;  
 Matches 157; Conservative 67; Mismatches 154; Indels 66; Gaps 17;

```

QY      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV 75
      | | : | : | | | : | : | : | : | : | : | : | : | : | : | : |
Db      288 CRP-----KLQCKSGFIQD-ALGNCDINECLSLISAPCPIGHTCINTEGSYTC----- 334

QY      76 YRGYPYNSPYSTPYSGPYAAAPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD 134
      : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db      335 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAFP 363

QY      135 SHQCNPTQICINTEGGYTCSTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS 189
      : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      364 AEPGKGHRCVNSPGSFRCECKTGYYFDGISRMCVDVNECQRYPGRLCGHKCENTLGSYL 423

QY      190 CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEB-DGVHCSDM 248
      | : | : | | : | | | : | : | : | : | : | : | : | : | : | : |
Db      424 CSCSVGFRLSVDGRSCDEINCSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDI 482

QY      249 DECSF--SEFLQHQRCVNQPGTYFCSCP-PGYILLDDNRSQDINECEHRNHTCNLQQT 305
      ||| : : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

**Zy**            23 AQAQCTNGFDLDRSQGCLDIDECRTIPEACRGDMMCVNQGYYLCIPRTNPVYRGPYSN      82  
       |::| :|| ::| :|::|::| :|::| :|::| :|  
**Dz**          829 ARQRCDMGF-LQDFEGNCVDINECTSLLPECRSGFGSCINTVGSSYTC----- 873  
  
**Zy**            83 PYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPT 141  
       : : : : : : : : : : : : : : : :



F;1-27/Domain: signal sequence #status predicted <SIG>  
 F;28-1184/Product: fibulin-2 protein #status predicted <MAT>  
 F;905-941/Domain: EGF homology <EGF>

Query Match 28.0%; Score 709.5; DB 2; Length 1184;  
 Best Local Similarity 34.3%; Pred. No. 5.1e-39;  
 Matches 146; Conservative 61; Mismatches 156; Indels 63; Gaps 12;

```

Qy      15 LCLPSPGN---AQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIP 70
      || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      780 LCQNTKGSFYQARQRCMDGF-LQDPEGNVCVDINECTSLSEPCRPFGFSCINTVGSYTC-- 836

Qy      71 RTNPVYRGPYSNPYSTPYSGPYAAAPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVD 129
      ||| | | | | | : : | : | : | : | : | : | : | : | : | : | : |
Db      837 -----QNRPLICARGYHASDDGAKCVDVN 860

Qy      130 ECATDSHQCNPTQICINTEGGYTCSCTDGYW--LLEGQCLDIDECRYG---YQQQLCANV 184
      || | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      861 ECETGVHRCGEGQVCHNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHTCENT 920

Qy      185 PGYSYCTCNPGFTLNEGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYLEEDGVH 244
      || | : | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db      921 LGSYRCSCASGFLLAADGKRCBDVNECEAQR-CSQECANIYGSYQCYCRQGYQLAEDGHT 979

Qy      245 CSDMDECS-FSEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQ 302
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      980 CTDIDECAQAGILCTFRCLNVPGSYQCACPEQGYTMTANGRSCKDVDECALGTHNCSEA 1039

Qy      303 QTCYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRD-----QPFTILYRDMDVV 356
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      1040 ETCHNIQGSFRCL-RFECPPNYVQVSKTKC---ERTTCHDFLECQNSPARITHYQLNFQ 1094

Qy      357 SGRSVPADIFQMQATTPYGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRI 416
      : | | | | : : : : : : : | : | : | : | : | : | : | : | : | : | : |
Db      1095 TGLLVPAHIFRIGPAPAFPTGDTIALNIKGNEEGYFGTTRRLNAYTGVVYLRQAVLEPRDF 1154

Qy      417 QLDLEM 422
      || : |
Db      1155 ALDVEM 1160
  
```

# RESULT 7

S34968

fibulin, splice form D precursor - mouse

N;Alternate names: basement-membrane protein BM-90; calcium-binding protein BM-90

C;Species: Mus musculus (house mouse)

C;Date: 10-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 02-Aug-2002

C;Accession: S34968; S36441; S13814

R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.

Eur. J. Biochem. 215, 733-740, 1993

A;Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent binding to other basement-membrane ligands.

A;Reference number: S34968; MUID:93358897; PMID:8354280

A;Accession: S34968

A;Molecule type: mRNA

A;Residues: 1-705 <PAN>



R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.  
submitted to the EMBL Data Library, January 1993  
A;Description: Sequence of extracellular mouse protein BM-90/fibulin and its  
calcium-dependent binding to other basement membrane ligands.  
A;Reference number: S36440  
A;Accession: S36441  
A;Molecule type: mRNA  
A;Residues: 1-39,'P',41-705 <PAW>  
A;Cross-references: EMBL:X70854; NID:g396820; PIDN:CAA50207.1; PID:g396821  
A;Experimental source: cell-line F9 teratocarcinoma  
R;Kluge, M.; Mann, K.; Dziadek, M.; Timpl, R.  
Eur. J. Biochem. 193, 651-659, 1990  
A;Title: Characterization of a novel calcium-binding 90-kDa glycoprotein (BM-90)  
shared by basement membranes and serum.  
A;Reference number: S13814; MUID:91065369; PMID:2249686  
A;Accession: S13814  
A;Molecule type: protein  
A;Residues: 28;31-49,'X',51-53;'XX',110-117;231-240,'X',242-243;339-362,'S',364-  
387;434-439;469-476;'Q',554-557;'Q',559-563;574-581 <KLU>  
C;Superfamily: fibulin-1; EGF homology  
C;Keywords: alternative splicing; basement membrane; calcium binding;  
extracellular matrix; glycoprotein; plasma  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-705/Product: fibulin, splice form D #status predicted <MAT>  
F;98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.8%; Score 703.5; DB 2; Length 705;  
Best Local Similarity 34.9%; Pred. No. 7.9e-39;  
Matches 162; Conservative 67; Mismatches 156; Indels 79; Gaps 22;

```

Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCMVNGGYLCIPRTNPV 75
      | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      290 CRP-----KLQCKSGFIQD-ALGNCIDINECLISAPCPVGQTCTINTEGSYTC----- 336

Qy      76 YRGPYSNPYSTPYSGPYPAAPPLSAFNPYPTISRPLICRFGYQM-DESNQCVDVDECATD 134
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      337 -----QKNVEN-----CGRGYHLNEEGTRCVDVDECAFP 365

Qy      135 SHQCNPQTQICINTEGGYTCSDTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS 189
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      366 AEPCKGKHHLNLSPGSPRCECKAGFYFDGISRTCTVDINECQRYPRGLCGHKCENTPGSFH 425

Qy      190 CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCPGYELEEE-DGVHCSDM 248
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      426 CSCSAGFRLSVDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDI 484

Qy      249 DECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTC 305
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      485 DECALPTGGHICSYRCINIPGSFQSCSPSSGYYRLAPNGRNCQDIDECVTGTIHNCSINET 544

Qy      306 YNLQGGFKCIDPIRCEEPYLRISDN-----RCM--CPAENPGC-RDQPPTILYRDM 353
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      545 FNIQGSFRCLSFECPENYRRSADTFRQEKTTDTRCISCRPNDEACVRDPVHTVSHTWI 603

Qy      354 DVVSGRSV--PADIFQMATT-RYPG--AYYIFQIKSGNEGREFYM---RQTGPISATLV 405
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      604 SLPTFRPFRPEEIIFLRAVTPLYPANQADIIFDITEGNLRDSFDIIKRYEDGMTVGVVR 663

```

```

Qy      406 MIRPIKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 448
          ||| ||   | |||   : |:: |  :|: : |::|:| |
Db      664 QVRPIVGPFYAVLKLENNYVLGGVVSRR--NVNVHIFVSEYWF 705

```

## RESULT 8

fibulin 1 precursor, splice form B - human

C;Date: 19-Apr-1991 #sequence revision 19-Apr-1991 #text change 02-Aug-2002

R; Argraves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.

A;Title: Fibulin is an extracellular matrix and plasma glycoprotein with repeated domain structure.

A;Accession: B36346

A;Residues: 1-601 <ARG>

C:Genetics:

A;Cross-references: GDB:278285; OMIM:135820

C; Superfamily: fibulin-1; EGF homology

F;180-214/Domain: EGF homology <EGF1>

51 2007

Query Match 24.4%; Score 619; DB 2; Length 601;  
Best Local Similarity 37.7%; Pred. No. 2.3e-33;  
Matches 121; Conservative 47; Mismatches 97; Indels 56; Gaps 13;

Qy 16 CLPSPGNAQAQCTNGFDLDRQSGQLDIDECRTIPEACRGDMMCVNQNNGYLCPRTNPV 75  
| | : || : | | :||:| | | :| |  
Db 288 CRP-----KLOCKSGFIOD-ALNCIDINECLSIAPCPIGHTCINTGYSYC----- 334

Qy 76 YRGPSYNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD 134  
: || | || : : | : |||||  
Db 335 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAAP 363

Qy 135 SHQCNP TQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS 189  
: | :|: | : | | | : : |::| | | | | | | |  
Db 364 AEPCKGKGRVCNPSGFRCECKTGYYFDGISRMCDVDNECORYPGRILCGHKCENTLGSYL 423

Qy 190 CTCNPGFTLLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDM 248  
|:|: || |: |||||:|:||||: :|| | | |||: | ||: | ||| | :  
Db 424 CSCSVGFRLSVDGRSCEDINECSS-SPCSQECANVYGSYOCYCRRGVOLSPVDGVTCEDI 482

```

Qy      249 DECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTC 305
      |||:      :| : |:| ||:: ||| | | : |:| |||:| | |:::| |
Db      483 DECALPTGGHICSYRCINIPGSFOCSCPSSGYRLAPNGRNCODIDECVTGIHNCSINETC 542

```

Qy 306 YNLQGGFKCIDPIRCEEPYLR 326  
:|:| | |:|: | | | |  
Db 543 FNIQGAFRCL-AFECPENYRR 562

RESULT 9

T42760

fibulin, splice form D precursor - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 23-Sep-2002

C;Accession: T42760

R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, W.S.

submitted to the EMBL Data Library, February 1998

A;Description: Isolation of chicken and nematode fibulin-1 homologs and characterization of the nematode fibulin-1 gene.

A;Reference number: Z22267

A;Accession: T42760

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-689 <BAR>

A;Cross-references: EMBL:AF051401; PIDN:AAC28321.1

C;Genetics:

A;Note: FBLN1

Query Match 23.9%; Score 606.5; DB 2; Length 689;  
Best Local Similarity 27.3%; Pred. No. 1.7e-32;  
Matches 159; Conservative 53; Mismatches 163; Indels 207; Gaps 20;

```

QY      15 LCLPSPG-NAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTN 73
      ||      |      :      :|||      :|||      :      :||      :      :||
Db      167 LCHDRGGGEKVCSCRSRSGFDLAPDGMACVDIDEACATLMDDCLESQRCLNTPGSFKCI---- 222

QY      74 PVYRGPSYNPYSTPYSGPYPAAPPLSAPNYPITISRLPICRFYQMD-ESNQCVVDDECA 132
      ||      |      ||      ||      ||      ||      ||      ||      ||      ||
Db      223 -----RTLSGCTGYAMDSETERCDVDECN 247

QY      133 TDSHQCNPTQICINTEGGYTC-----SCTDGYWLLEGQCLDIDE 171
      ||      |      ||      ||      ||      ||      :||      :||      ||      ||
Db      248 LGSHDGGLYQCRNTQGSYRCDAKKCGDGELQNPMTGECTSITCPNGYYPKNGMCNDIDE 307

QY      172 CRYGY-----CQQ---LCA-----N 183
      |      :||      ||      ||
Db      308 CVTGHNCGAGEBCVNTPGSFRCCQKGNLCAHGYEVNGATGFCEVDNECQQGVCGSMECIN 367

QY      184 VPGSYSCTCNPGFTLNE-----200
      :||      |      ||      :||
Db      368 LPGTGYCKOGPGYEFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFCECKCKPGFQLA 427

QY      201 -DGRSCQDVNECATE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSF----S 254
      ||      :|||      ||      ||      ||      ||      ||      ||      ||      ||
Db      428 SDGRRCEDVNECTTGIAACEQKCVNIPGSYQICIDRGFALGPDGTCEDIDECISIWAGSG 487

QY      255 EFLQCHECVNPGTYFCSCPYPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKC 314
      ||      :||      :||      ||      ||      :||      :||      :||      ||      ||
Db      488 NDLCMGGCINTKGSYLCQCPPGYKIQFDGRTCDVDDECA-MGECAGSDKVCVNTLGSFKC 546

QY      315 IDPIRCEEPLYLRISDNR-----C--MCPAENPGC-RDPFTILYRMDVVSGRSV-- 361
      ||      |      :||      :||      :||      :||      :||      :||      :||
Db      547 -HSIDCPTNYIHDSLKNQIADGYSCIKVCSTEDTECLGNHTREVLYQFRAVPSLKTIIIS 605

```





QY 183 NVPGSYSCTCNPGFTLINE----- 200  
 Db 267 NLPGTYKCKCGPGYEFNDACKRCEDVDECIKFAHVCDDLAEICINTIGSFCECKCKPGFQL 326

QY 201 --DGRSCQDVNECATE--NPCVQTCVNTYGSFICRCDPGYELBEDGVHCSMDMECSF---- 253  
 Db 327 ASDGRRCEDVNECTTGIAACEQKCVNI PGSYQCICDRGFALGPDGKCEDIDECISIWAGS 386

QY 254 SEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFK 313  
 Db 387 GNDLCMGGCINTKGSYLCQCFPGYKIQPDGRTCVDVDECA--MGECAGSDKVCVNTLGSFK 445

QY 314 CIDPIRCEEPYLRI SDNR-----C--MCPAENPGC-RDQPTTILYRDMVVSGRSV- 361  
 Db 446 C-HSIDCPTNYIHDSLANKNQIADGYSCIKVCSTEDTECLGNHTREVLYQFRAVPSLKTII 504

QY 362 -PADI-----FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPI 410  
 Db 505 SPIEVSRIVTHMGVPPFSVDYNLDYVGQRHFRIVQERNIG-----IVQLVKPI 551

QY 411 KGPREIQLDLEMITVNTVINFRGSSVIR----LRIVVSQYPF 448  
 Db 552 SGP----TVETIKVNIHTKSRTGVILAFNEAIEISVSKYPF 589

# RESULT 12

T22793

hypothetical protein F56H11.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 02-Aug-2002

C;Accession: T22793; T24489

R;Wilkinson, J.

submitted to the EMBL Data Library, January 1996

A;Reference number: Z19616

A;Accession: T22793

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-798 <WIL>

A;Cross-references: EMBL:Z68749; PIDN:CAA92962.1; GSPDB:GN00022; CESP:F56H11.1

A;Experimental source: clone F56H11

R;Lloyd, C.

submitted to the EMBL Data Library, December 1995

A;Reference number: Z19897

A;Accession: T24489

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-798 <WI2>

A;Cross-references: EMBL:Z68219; PIDN:CAA92483.1; GSPDB:GN00022; CESP:F56H11.1

A;Experimental source: clone T05A1

C;Genetics:

A;Gene: CESP:F56H11.1

A;Map position: 4

A;Introns: 14/1; 92/3; 144/1; 195/1; 281/1; 325/2; 371/2; 390/1; 437/1; 471/3; 498/3; 607/1; 649/2; 718/1

C;Superfamily: fibulin-1; EGF homology

Query Match 22.8%; Score 577.5; DB 2; Length 798;  
 Best Local Similarity 26.7%; Pred. No. 1.6e-30;  
 Matches 162; Conservative 50; Mismatches 180; Indels 215; Gaps 23;

```

QY      15 LCLPSPG-NAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMCMVNQNGGYLC----- 68
      || | | | : | : || | | : | : | | | | | | | | | |
Db      167 LCHDRGGEKVECSRSGFDLAPDGMACVDRNECLTRQSPCTQSEDCVNTIGGYICQRRIS 226

QY      69 --IP---RTNPVYRGP---YSNPYSTPYSGPYAAAPP----- 98
      : | | | : | : | | | : | | | : | | |
Db      227 RLVPHRHRANRIGNAPRRMRDDPYSR--AGEYREASQANTEFGCPMGWLFQHGHCVDIDE 284

QY      99 -----LSAPNYPTISRPLICRFGYQMD---ESNQCV----- 126
      : | | | | | | | | | | | | | | | |
Db      285 CATLMDDCLESQRCINTPGSPFKCIRTLSCTGYAMDSETERNNCFILINNTFNCKYFPV 344

QY      127 -DVDECATDSHQCNPTQICINTEGGYTCS----- 154
      || | | | | | | | | | | | | | | | |
Db      345 EDVDECNLGSHDGPLYQCRNTQGSYRCDAKKCGDGLQNPMTGEYIDECVTGHNCGAGE 404

QY      155 -----CTDGYWL--LEGQCLDIDECRYGYCQQL--CANVPGSYSTCTNP 194
      | | | : | | : | | : | | : | | : | | : | |
Db      405 ECVNTPGSFRCCQKGNLCAHGYEVNGATGFCEDVNECQQGVCGSMBCINLPGTYKCKCGP 464

QY      195 GFTLNE-----DGRSCQDVNE 210
      | : | | | | | | | | | | | | | |
Db      465 GYEFNDAKKRCEVDVECIKFAGHVCDLSAECINTIGSFCECKPGFQLASDGRRCEDVNE 524

QY      211 CATE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSF---SEFLCQHECVNQ 265
      | | | | | | | | | | | | | | | | | | | |
Db      525 CTTGIAACBQKCVNIPGSYQICDRGFALGPDGTKCEDIDBCSIWAGSGNDLCMGGCINT 584

QY      266 PGTYFCSCPFGYIILLDDNRSCQDINECEHRNHTCNLQQTCTYNLQGGFKCIDPIRCEEPYL 325
      | : | | | | | | : | | : | | : | | : | | : | |
Db      585 KGSYLQCPFGYKIQPDGRTCDVDVDECA-MGECAGSDKVCVNTLGSFKC-HSIDCPNTNYI 642

QY      326 RISDNR-----CMCPAENPGCRDQPFITLYRDMVVSGRSVP----- 362
      | | : | | | | | | | | | : | : : | : |
Db      643 HDSLKNRNCNRQPSACGLPEB---CSKVPLFLTYQFISL--ARAVPISSHRPAITLFKVS 697

QY      363 ----ADI---FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTPG--ISATLVMTRPIKGP 413
      | | | : | | : | | : | | : | | : | | : | |
Db      698 APNHADTEVNFEQLKTTIVGAPNVLPAIRAN----FLLQKGEKRN SAVVTLRDSL DGP 752

QY      414 REIQLDL 420
      : : | |
Db      753 QTVKLQL 759
  
```

# RESULT 13

A35626

transforming growth factor beta-1-binding protein - human

C:Species: Homo sapiens (man)

C>Date: 21-Sep-1990 #sequence\_revision 21-Sep-1990 #text\_change 11-Jan-2000

C:Accession: A35626

R;Kanzaki, T.; Olofsson, A.; Moren, A.; Wernstedt, C.; Hellman, U.; Miyazono, K.; Claesson-Welsh, L.; Heldin, C.H.

Cell 61, 1051-1061, 1990

A;Title: TGF-beta1 binding protein: a component of the large latent complex of TGF-beta1 with multiple repeat sequences.

A;Reference number: A35626; MUID:90275601; PMID:2350783

A;Accession: A35626

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-1394 <KAN>

A;Cross-references: GB:M34057; NID:g339547; PIDN:AAA61160.1; PID:g339548

C;Superfamily: unassigned EGF-related proteins; EGF homology

C;Keywords: alternative splicing

F;750-791/Domain: EGF homology <EGF>

Query Match 21.5%; Score 544; DB 2; Length 1394;

Best Local Similarity 29.4%; Pred. No. 4e-28;

Matches 128; Conservative 52; Mismatches 134; Indels 122; Gaps 17;

```
Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDI DECR TIPEACRGMVCNVQNGGYLCI PRTNPV 75
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      562 CINLPVRYTCICYEGYRFSEQQRKCVDI DECT QVQHLC-SQGRCENTEGSF LCI----- 614

Qy      76 YRGPYSNPYSTPYSGPYFAAAPLSAPNYPTI SRPLI-----CRFGYQ 118
      : | : : : : : : : : : : : : : : : : : : : : : :
Db      615 -----CPAGFMASEEGTNCIDVDECLRPDVC GEGHCVNTVGA PRCEYCDSGYR 662

Qy     119 MDES NQCV DVECATD SHQCNPTQICINTEGGYTC-SCTDGYWLL EGQCLDI DEC-RYGY 176
      | : : | | | | | | | | | : | : | | | | | | | | | | | |
Db     663 MTQRGR CEDIDECLNPS-TC-PDEQCVNSPFGSYQCVPTCTEGFRGWNGQCLD VDECLPNV 720

Qy     177 CQQ-LCANVP GSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQ-----219
      | : | : | | | | | | | | | : | : | | | | | | | | | |
Db     721 CANGDCSNLEGSYMC SCHKGYTRTPDHKHC RDIDE CQQGNLCVNGQCKNTEG SFRC TCGQ 780

Qy     220 -----TCVNTYGSFICRCDPGYELEEDGVHCS DMDECSF 253
      | | | | | | | | | | | | | | | | | | | | | |
Db     781 GYQLSAAKQ CEDIDE CQHRHLCAHGQCRNTEG SFQCVCDQGYRASGLGDHCE DINECLE 840

Qy     254 SEFLCQH-ECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGF 312
      : | | : | | | | | | | | | | | | | | | | | | | | |
Db     841 DKSVCQRGDCINTAGSYDCTCPDGF-QLDDNKTCQDINECEHPG-LCGPQGECLNTEG SF 898

Qy     313 KCI-----DPIRCEEPYLRI S-----DN-----RCMC-----PAENPGCR 342
      | : | | | | | | | | | : : | | | | | | | | | | |
Db     899 HCV CQQGFSISADGRT CEDIDE CVNNTVCD SHGFC DNTAGSFRCLCYQG FQAPQDGQCV 958

Qy     343 DQPFTILYRDM DVVSG 358
      | : : : : : : : : : : : : : : : : : : : : :
Db     959 D-----VNECELLSG 968
```

RESULT 14

A47221

fibrillin 1 precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jun-1995 #sequence revision 25-Apr-1997 #text\_change 02-Aug-2002

C;Accession: A47221; I54355; S17064; I59574; S17062; S62111; A34198

R;Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.



Genomics 17, 476-484, 1993

A;Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure and alternatively spliced exons at the 5' end.

A;Reference number: A47221; MUID:94010947; PMID:7691719

A;Accession: A47221

A;Molecule type: mRNA

A;Residues: 1-337,'T',339-1029 <COR>

A;Cross-references: GB:X63556

R;Pereira, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Pangilinan,

T.; Bonadio, J.

Hum. Mol. Genet. 2, 961-968, 1993

A;Title: Genomic organization of the sequence coding for fibrillin, the defective gene product in Marfan syndrome.

A;Reference number: I54355; MUID:93372860; PMID:8364578

A;Accession: I54355

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 132-3002 <PER>

A;Cross-references: GB:L13923; NID:g306745; PIDN:AAB02036.1; PID:g306746

R;Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y.

Nature 352, 334-337, 1991

A;Title: Partial sequence of a candidate gene for the Marfan syndrome.

A;Reference number: S17064; MUID:91304568; PMID:1852207

A;Accession: S17064

A;Molecule type: mRNA

A;Residues: 1030-3002 <MAS>

A;Cross-references: EMBL:X63556

R;Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J.

Science 259, 680-683, 1993

A;Title: The skipping of constitutive exons in vivo induced by nonsense mutations.

A;Reference number: I59574; MUID:93157831; PMID:8430317

A;Accession: I59574

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 2217-2288,'I',2290-2325 <RES>

A;Cross-references: GB:S54426; NID:g264860; PIDN:AAB25244.1; PID:g264861

R;Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.;

Tsipouras, P.; Ramirez, F.; Hollister, D.W.

Nature 352, 330-334, 1991

A;Title: Linkage of Marfan syndrome and a phenotypically related disorder to two different fibrillin genes.

A;Reference number: S17062; MUID:91304567; PMID:1852206

A;Accession: S17062

A;Molecule type: mRNA

A;Residues: 'VLVTVVFIFLSYNKML',944-1444 <LEE1>

A;Cross-references: EMBL:X62008; NID:g31398; PIDN:CAB56534.1; PID:g5924015

A;Accession: S62111

A;Molecule type: protein

A;Residues: 1166-1176,'X',1178-1180,'D',1182-1185 <LEE2>

R;Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.

J. Biol. Chem. 264, 21381-21385, 1989

A;Title: Connective tissue microfibrils. Isolation and characterization of three large pepsin-resistant domains of fibrillin.

A;Reference number: A34198; MUID:90078246; PMID:2512293

A;Accession: A34198

A;Molecule type: protein

A;Residues: 565-575;1890-1892,'I',1894-1900 <MAD>  
 C;Comment: Fibrillin is a major component of elastin-associated microfibrils.  
 C;Genetics:  
 A;Gene: GDB:FBN1  
 A;Cross-references: GDB:127115; OMIM:134797; OMIM:154700  
 A;Map position: 15q21.1-15q21.1  
 A;Introns: 2236/1; 2258/1; 2297/1  
 C;Superfamily: fibrillin 1; EGF homology  
 C;Keywords: alternative splicing; calcium binding; extracellular matrix;  
 glycoprotein; Marfan syndrome  
 F;1-3002/Product: fibrillin (5'-region exon A splice form) (fragment) #status  
 predicted <MATA>  
 F;132-3002/Product: fibrillin (5'-region exon C splice form) #status predicted  
 <MATC>  
 F;1332-1367/Domain: EGF homology <EGF>  
 F;1457-1492/Domain: EGF homology <EGF2>  
 F;2262-2295/Domain: EGF homology <EGF1>

Query Match 21.0%; Score 532.5; DB 2; Length 3002;  
 Best Local Similarity 30.1%; Pred. No. 4.5e-27;  
 Matches 124; Conservative 50; Mismatches 125; Indels 113; Gaps 18;

```

Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQLDIDECRTIPEACRGDMMCVNQGGYLCIPRTNPV 75
      | : | : : | : | | : | | | | | | : | | | | : | : :
Db      1175 CRNTIGSFKCRCDSGFALDSEERNCTDIDECRISPDLG-GRGQCVNTPGDFEC--KCDEG 1231

Qy      76 YRGPSYNPYSTPYSGPYAAAPLSAPNYPTISR----PLICRF----- 115
      | : | : | : | : | | | | | | | | | | | | | | | |
Db      1232 YESGF-----MMMNKNCMDIDECQRDPLLCRGGVCHNTEGYSRCECP 1273

Qy      116 GYQMDES-NQCVDVDCAETDSSHQCNPTQICINTEGGYTCSDTGYWLLLEGQ--CLDIDEC 172
      | : | : : | : | | : | | | | | : | | | | | : | : | | |
Db      1274 GHQLSPNISACIDINECELSAHLG-PNGRCVNLIGKYQCACNPGYHSTPDRLFQVDIDEC 1332

Qy      173 RY--GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENP----- 216
      | | : | | | | | | | | | | | | | | | | | | | |
Db      1333 SIMNGGCETFTCTNSEGSYECSCQPGFALMPDQRSCTDIDEC-EDNPNICDGGQCTNIPGE 1391

Qy      217 -----CVQ-----TCVNTYGSFICRCDPGYELEEDGVHC 245
      | | | | | | | | | | | | | | | | | | | | |
Db      1392 YRCLCYDGMASEDMKTCVDVNECDLNPNICLSGTCENTKGSFICHDGMGYSKKGKTGC 1451

Qy      246 SDMDECSFSEFLC-QHE-CVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQ 303
      | : | | | | | | | | : | | | | | | | | | | : | : |
Db      1452 TDINECRIGAHNCGKHAVCTNTAGSFKSCSPGWT--GDGIKCTDLDECSNGTHMCSQHA 1509

Qy      304 TCYNLQGGPKCIDPIRCBEPYL-----RISDNRCMPAENPGCRDQP 345
      | | | : | : | : | | | | | | | | | | | | |
Db      1510 DCKNTMGSYRCL---CKEGYTGDTCTDLDECSENLNLG--GNGQCLNAP 1555

```

# RESULT 15

A55567  
 fibrillin I - bovine  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 02-Aug-2002  
 C;Accession: A55567

R;Tilstra, D.J.; Li, L.; Potter, K.A.; Womack, J.; Byers, P.H.  
Genomics 23, 480-485, 1994

A;Title: Sequence of the coding region of the bovine fibrillin cDNA and localization to bovine chromosome 10.

A;Reference number: A55567; MUID:95137597; PMID:7835900

A;Accession: A55567

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-2871 <TIL>

A;Cross-references: GB:L28748; NID:g508427; PIDN:AAA74122.1; PID:g508428

C;Superfamily: fibrillin 1; EGF homology

F;1201-1236/Domain: EGF homology <EGF>

Query Match 21.0%; Score 531.5; DB 2; Length 2871;

Best Local Similarity 29.6%; Pred. No. 5e-27;

Matches 122; Conservative 48; Mismatches 129; Indels 113; Gaps 16;

```
Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNFV 75
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      1044 CRNTIGSFKRCRCDSGFALDSEERNCTDIDECRISPDLC-GRGQCQVNTPGDFEC--KCDEG 1100

Qy      76 YRGPYSNPYSTPYSGPYPAAPPLSAFNYPTISR---PLICRFGYQMDES----- 122
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      1101 YESGF-----MMMKNCMDIDECQRDPLLCRGGVCINTEGSYRCECPP 1142

Qy      123 -----NQCVDVDECATDSDHQCNPQTQICINTEGGYTCSCTDGYWLLLEGQ--CLDIDEC 172
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      1143 GHQLAPNISACIDINECELSAHL-C-PHGRCVNLIGKYQCACNPGYHSTPDRLFCVDIDEC 1201

Qy      173 RY--GYCQQLCANVPGSYSCNPFGLTNEEDGRSCQDVNECATENP----- 216
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      1202 SIMNGGCETFTCTNSEGSYECSCQPGFALMPDQRSCTDIDBC-EDNPNICDGGQCTNIPGE 1260

Qy      217 -----CVQ-----TCVNTYGSFICRCDPGYELEEDGVHC 245
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      1261 YRCLCYDGFMASEDMMKTCVDVNECDLNPNICLSGTCENTKGSFICDCMDMGYSGKKGKTC 1320

Qy      246 SDMDECSFSEFLCQHE--CVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCNLQQ 303
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      1321 TDINECEIGAHNCDRHAVCNTNTAGSFKCSCSPGWI--GDGIKCTDLDECSNGTHMCSQHA 1378

Qy      304 TCYNLQGGFKCIDPIRCEEPYL-----RISDNRCMCPAENPGCRDQP 345
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      1379 DCKNTMGSYRCL---CKEGYTGDFCTDLDECSENLNL--GNGQCINAP 1424
```

Search completed: January 9, 2004, 12:34:53

Job time : 19.9736 secs

OM protein - protein search, using sw model

Run on: January 9, 2004, 12:21:36 ; Search time 10.287 Seconds  
(without alignments)  
2048.013 Million cell updates/sec

Title: US-09-674-379A-13  
Perfect score: 2533  
Sequence: 1 MPGIKRILTVTILALCLPSP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2533	100.0	448	1	FBL5_HUMAN	Q9ubx5 homo sapien
2	2406	95.0	448	1	FBL5_RAT	Q9wvh8 rattus norv
3	2405	94.9	448	1	FBL5_MOUSE	Q9wvh9 mus musculu
4	1290	50.9	443	1	FBL4_CRIGR	O55058 cricetulus
5	1289	50.9	443	1	FBL4_HUMAN	O95967 homo sapien
6	1282	50.6	443	1	FBL4_MOUSE	Q9wvj9 mus musculu
7	1109.5	43.8	493	1	FBL3_RAT	Q35568 rattus norv
8	1101	43.5	493	1	FBL3_HUMAN	Q12805 homo sapien
9	733.5	29.0	1221	1	FBL2_MOUSE	P37889 mus musculu
10	728	28.7	598	1	FBL1_CERAE	Q8mj99 cercopithec
11	722	28.5	704	1	FBL1_CHICK	O73775 gallus gall
12	709.5	28.0	1184	1	FBL2_HUMAN	P98095 homo sapien
13	701.5	27.7	703	1	FBL1_HUMAN	P23142 homo sapien
14	700.5	27.7	705	1	FBL1_MOUSE	Q08879 mus musculu
15	631	24.9	681	1	FBL1_BRARE	O42182 brachydanio
16	577.5	22.8	798	1	FBL1_CAEEL	O77469 caenorhabdi
17	544	21.5	1394	1	LTBS_HUMAN	P22064 homo sapien

18	544	21.5	1595	1	LTBL_HUMAN	Q14766	homo sapien
19	532.5	21.0	2871	1	FBN1_HUMAN	P35555	homo sapien
20	531.5	21.0	2871	1	FBN1_BOVIN	P98133	bos taurus
21	525.5	20.7	2871	1	FBN1_PIG	Q9tv36	sus scrofa
22	523	20.6	1712	1	LTB1_RAT	Q00918	rattus norv
23	521	20.6	1389	1	LTBS_MOUSE	Q8cgl8	mus musculus
24	521	20.6	1713	1	LTBL_MOUSE	Q8cgl9	mus musculus
25	518.5	20.5	2871	1	FBN1_MOUSE	Q61554	mus musculus
26	518.5	20.5	2907	1	FBN2_MOUSE	Q61555	mus musculus
27	517.5	20.4	2911	1	FBN2_HUMAN	P35556	homo sapien
28	475	18.8	956	1	MTN2_HUMAN	O00339	homo sapien
29	452	17.8	956	1	MTN2_MOUSE	O08746	mus musculus
30	421	16.6	931	1	EMR1_MOUSE	Q61549	mus musculus
31	392	15.5	886	1	EMR1_HUMAN	Q14246	homo sapien
32	379	15.0	2470	1	NTC2_MOUSE	O35516	mus musculus
33	377	14.9	2471	1	NTC2_HUMAN	Q04721	homo sapien
34	375	14.8	810	1	NEL1_HUMAN	Q92832	homo sapien
35	372.5	14.7	816	1	NEL2_MOUSE	Q61220	mus musculus
36	371.5	14.7	2471	1	NTC2_RAT	Q99w30	rattus norv
37	366	14.4	816	1	NEL2_HUMAN	Q99435	homo sapien
38	364	14.4	810	1	NEL1_RAT	Q62919	rattus norv
39	360.5	14.2	816	1	NEL_CHICK	Q90827	gallus gall
40	359.5	14.2	1964	1	NTC4_MOUSE	P31695	mus musculus
41	359	14.2	816	1	NEL2_RAT	Q62918	rattus norv
42	356	14.1	2703	1	NOTC_DROME	P07207	drosophila
43	355.5	14.0	2437	1	NTC1_BRARE	P46530	brachydanio
44	350.5	13.8	652	1	CD93_HUMAN	Q9npy3	homo sapien
45	347.5	13.7	2556	1	NTC1_HUMAN	P46531	homo sapien

# ALIGNMENTS

## RESULT 1

### FBL5\_HUMAN

ID FBL5\_HUMAN STANDARD; PRT; 448 AA.  
AC Q9UBX5; 075966;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest  
DE EGF-like protein) (Dance) (Urine p50 protein) (UP50).  
GN FBLN5 OR DANCE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Melanoma;  
RA Kostka G.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99357779; PubMed=10428823;  
RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,  
RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,

RA Matsumori A., Sasayama S., Chien K.R., Honjo T.;  
 RT "DANCE, a novel secreted RGD protein expressed in developing,  
 RT atherosclerotic, and balloon-injured arteries.";   
 RL J. Biol. Chem. 274:22476-22483 (1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Urine;  
 RA Zemel R., Sholto O., Shaul Y.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH  
 CC INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR  
 CC LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR  
 CC DEVELOPMENT AND REMODELING.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN HEART, OVARY, AND  
 CC COLON BUT ALSO IN KIDNEY, PANCREAS, TESTIS, LUNG, AND PLACENTA.  
 CC NOT DETECTABLE IN BRAIN, LIVER, THYMUS, PROSTATE, OR PERIPHERAL  
 CC BLOOD LEUKOCYTES.  
 CC -!- SIMILARITY: Belongs to the fibulin family.  
 CC -!- SIMILARITY: Contains 6 EGF-like domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AJ133490; CAB38568.1; -.  
 DR EMBL; AF112152; AAD41768.1; -.  
 DR EMBL; AF093118; AAC62107.1; -.  
 DR HSSP; P00736; 1APQ.  
 DR Genew; HGNC:3602; FBLN5.  
 DR MIM; 604580; -.  
 DR GO; GO:0005578; C:extracellular matrix; TAS.  
 DR GO; GO:0005625; C:soluble fraction; TAS.  
 DR GO; GO:0005178; F:integrin binding activity; TAS.  
 DR GO; GO:0007160; P:cell-matrix adhesion; TAS.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001881; EGF\_CA.  
 DR InterPro; IPR006209; EGF\_like.  
 DR Pfam; PF00008; EGF; 4.  
 DR SMART; SM00179; EGF\_CA; 4.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 4.  
 DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE; PS01186; EGF\_2; 4.  
 DR PROSITE; PS01187; EGF\_CA; 6.  
 KW Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;  
 KW Glycoprotein.  
 FT SIGNAL 1 23 POTENTIAL.  
 FT CHAIN 24 448 FIBULIN-5.  
 FT DOMAIN 24 69 EGF-LIKE 1, DIVERGENT.  
 FT DOMAIN 127 167 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 168 206 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 207 246 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 247 287 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

FT	DOMAIN	288	333	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	SITE	54	56	CELL ATTACHMENT SITE (POTENTIAL).
FT	DISULFID	131	144	BY SIMILARITY.
FT	DISULFID	138	153	BY SIMILARITY.
FT	DISULFID	155	166	BY SIMILARITY.
FT	DISULFID	172	181	BY SIMILARITY.
FT	DISULFID	177	190	BY SIMILARITY.
FT	DISULFID	192	205	BY SIMILARITY.
FT	DISULFID	211	221	BY SIMILARITY.
FT	DISULFID	217	230	BY SIMILARITY.
FT	DISULFID	232	245	BY SIMILARITY.
FT	DISULFID	251	262	BY SIMILARITY.
FT	DISULFID	258	271	BY SIMILARITY.
FT	DISULFID	273	286	BY SIMILARITY.
FT	DISULFID	292	305	BY SIMILARITY.
FT	DISULFID	299	314	BY SIMILARITY.
FT	DISULFID	320	332	BY SIMILARITY.
FT	CARBOHYD	283	283	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	296	296	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	69	70	IP -> HS (IN REF. 3).
FT	CONFLICT	147	148	TE -> MK (IN REF. 3).
SQ	SEQUENCE	448 AA; 50180 MW;		19PCA51FDA328003 CRC64;

Query Match 100.0%; Score 2533; DB 1; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-180;  
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV	60
Db	1	MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV	60
Qy	61	NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD	120
Db	61	NQNGGYLCIPRTNPVYRGFYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD	120
Qy	121	ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLBGQCLDIDECRYGYCQQL	180
Db	121	ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLBGQCLDIDECRYGYCQQL	180
Qy	181	CANVPGSYSTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE	240
Db	181	CANVPGSYSTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE	240
Qy	241	DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN	300
Db	241	DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCN	300
Qy	301	LQQTCTNQLQGGFKCIDPIRCEEPYLIRISDNRCMCPAENPGCRDQPFITLYRDMDVVSGRS	360
Db	301	LQQTCTNQLQGGFKCIDPIRCEEPYLIRISDNRCMCPAENPGCRDQPFITLYRDMDVVSGRS	360
Qy	361	VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRIKGPRIQLDL	420
Db	361	VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRIKGPRIQLDL	420
Qy	421	EMITVNTVINFRGSSVIRLRIYVSQYPF	448

## RESULT 2

## FBL5\_RAT

ID FBL5\_RAT STANDARD; PRT; 448 AA.  
AC Q9WVH8; Q9R284;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest  
DE EGF-like protein) (Dance) (Embryonic vascular EGF repeat-containing  
DE protein) (EVEC).  
GN FBLN5 OR DANCE.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;

## RN

[1]

## RP SEQUENCE FROM N.A.

RX MEDLINE=99357779; PubMed=10428823;  
RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,  
RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,  
RA Matsumori A., Sasayama S., Chien K.R., Honjo T.;  
RT "DANCE, a novel secreted RGD protein expressed in developing,  
RT atherosclerotic, and balloon-injured arteries.";  
RL J. Biol. Chem. 274:22476-22483(1999).

## RN

[2]

## RP SEQUENCE FROM N.A.

RX MEDLINE=99278197; PubMed=10347091;  
RA Kowal R.C., Richardson J.A., Miano J.M., Olson E.N.;  
RT "EVEC, a novel epidermal growth factor-like repeat-containing protein  
RT upregulated in embryonic and diseased adult vasculature.";  
RL Circ. Res. 84:1166-1176(1999).

CC -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH  
CC INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR  
CC LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR  
CC DEVELOPMENT AND REMODELING.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the fibulin family.

CC -!- SIMILARITY: Contains 6 EGF-like domains.

## CC

CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; AF112153; AAD41769.1; -.

DR EMBL; AF137350; AAD25101.1; -.

DR HSSP; P00736; 1APQ.

DR InterPro; IPR000152; Asx\_hydroxyl.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR006209; EGF\_like.

DR Pfam; PF00008; EGF; 4.





```

Db      241  DGIHCSDMDECSFSEFLCQHECVNQPGSYFCSCPPGYVLLEDNRSCQDINECEHRNHTCT 300
Qy      301  LQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMVVSGRS 360
Db      301  PLQTCYNLQGGFKCIDPIVCEEPYLLIGDNRCMCPAENTGCRDQPFITILFRDMVVSGRS 360
Qy      361  VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
Db      361  VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
Qy      421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
Db      421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448

```

# RESULT 3

## FBL5\_MOUSE

```

ID      FBL5_MOUSE      STANDARD;      PRT;      448 AA.
AC      Q9SVH9;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest
DE      EGF-like protein) (Dance).
GN      FBLN5 OR DANCE.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99357779; PubMed=10428823;
RA      Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
RA      Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
RA      Matsumori A., Sasayama S., Chien K.R., Honjo T.;
RT      "DANCE, a novel secreted RGD protein expressed in developing,
RT      atherosclerotic, and balloon-injured arteries.";
RL      J. Biol. Chem. 274:22476-22483(1999).
CC      -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
CC      INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
CC      LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
CC      DEVELOPMENT AND REMODELING.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- SIMILARITY: Belongs to the fibulin family.
CC      -!- SIMILARITY: Contains 6 EGF-like domains.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL; AF112151; AAD41767.1; -.
DR      HSSP; P00736; 1APQ.

```





```

InterPro; IPR001491; Thrbomodulun.
DR Pfam; PF00008; EGF; 4.
DR PRINTS; PR00907; THRMBOMODULN.
DR SMARTS; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS01187; EGF_CA; 6.
KW Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 443 EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
FT MATRIX PROTEIN 2.
FT DOMAIN 36 81 EGF-LIKE 1, DIVERGENT.
FT DOMAIN 123 163 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 164 202 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 203 242 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 243 282 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 283 328 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DISULFID 127 140 BY SIMILARITY.
FT DISULFID 134 149 BY SIMILARITY.
FT DISULFID 151 162 BY SIMILARITY.
FT DISULFID 168 177 BY SIMILARITY.
FT DISULFID 173 186 BY SIMILARITY.
FT DISULFID 188 201 BY SIMILARITY.
FT DISULFID 207 217 BY SIMILARITY.
FT DISULFID 213 226 BY SIMILARITY.
FT DISULFID 228 241 BY SIMILARITY.
FT DISULFID 247 258 BY SIMILARITY.
FT DISULFID 254 267 BY SIMILARITY.
FT DISULFID 269 281 BY SIMILARITY.
FT DISULFID 287 300 BY SIMILARITY.
FT DISULFID 294 309 BY SIMILARITY.
FT DISULFID 315 327 BY SIMILARITY.
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 443 AA; 49432 MW; 08CFE5D7323D9E5F CRC64;

```

[illegible]



RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the fibulin family.

CC -!- SIMILARITY: Contains 6 EGF-like domains.

CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL; AJ132819; CAA10791.2; -.

DR EMBL; AF093119; AAC62108.1; -.

DR EMBL; AF109121; AAF65188.1; -.

DR EMBL; BC010456; AAH10456.1; -.

DR HSSP; P35555; 1EMN.

DR Genew; HGNC:3219; EFEMP2.

DR MIM; 604633; -.

DR GO; GO:0005604; C:basement membrane; TAS.

DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.

DR InterPro; IPR000152; Asx\_hydroxyl.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR006209; EGF\_like.

DR InterPro; IPR001491; Thrbomoduln.

DR Pfam; PF00008; EGF; 4.

DR PRINTS; PR00907; THRMBOMODULN.

DR SMART; SM00179; EGF\_CA; 4.

DR PROSITE; PS00010; ASX\_HYDROXYL; 4.

DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.

DR PROSITE; PS01186; EGF\_2; 4.

DR PROSITE; PS01187; EGF\_CA; 6.

KW Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.

FT SIGNAL 1 25 POTENTIAL.

FT CHAIN 26 443 EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR  
 FT MATRIX PROTEIN 2.

FT DOMAIN 36 81 EGF-LIKE 1, DIVERGENT.

FT DOMAIN 123 163 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 164 202 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 203 242 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

FT	DOMAIN	243	282	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	283	328	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	DISULFID	127	140	BY SIMILARITY.
FT	DISULFID	134	149	BY SIMILARITY.
FT	DISULFID	151	162	BY SIMILARITY.
FT	DISULFID	168	177	BY SIMILARITY.
FT	DISULFID	173	186	BY SIMILARITY.
FT	DISULFID	188	201	BY SIMILARITY.
FT	DISULFID	207	217	BY SIMILARITY.
FT	DISULFID	213	226	BY SIMILARITY.
FT	DISULFID	228	241	BY SIMILARITY.
FT	DISULFID	247	258	BY SIMILARITY.
FT	DISULFID	254	267	BY SIMILARITY.
FT	DISULFID	269	281	BY SIMILARITY.
FT	DISULFID	287	300	BY SIMILARITY.
FT	DISULFID	294	309	BY SIMILARITY.
FT	DISULFID	315	327	BY SIMILARITY.
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	394	394	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	5	5	A -> T (IN REF. 1).
FT	CONFLICT	44	51	EWDPDSQH -> TQTAN (IN REF. 2).
FT	CONFLICT	103	111	AQHFNPCPP -> VNTQPLPT (IN REF. 2).
FT	CONFLICT	294	294	C -> W (IN REF. 2).
FT	CONFLICT	354	356	RSV -> AER (IN REF. 2).
FT	CONFLICT	355	355	S -> R (IN REF. 3).
SQ	SEQUENCE	443 AA;	49391 MW;	9E9AC2393780D3B8 CRC64;

Query Match 50.9%; Score 1289; DB 1; Length 443;  
 Best Local Similarity 49.9%; Pred. No. 1.7e-88;  
 Matches 226; Conservative 74; Mismatches 131; Indels 22; Gaps 5;

Qy	1	MPGIKRILTVTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG	55
Db	8	LPGSLLLWALLLLLIGSASPQDSEEPDSYTECTDGYEWDPPDSQHCRTVNECLTIPEACKG	67
Qy	56	DMMCVNQNGGYLCIPRTNPVYRGPYSNPFYSTPYSGPYPAAPPLSAPNYPTISRPLICRF	115
Db	68	EMKCNHYGGYLCILPRAAVINDLHG-----EGP-PPVPVPAQHFN-----PCPP	111
Qy	116	GYQMDESNQCDVDDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYG	175
Db	112	GYEPDDQDSCVDVDECAQALHDCRPSQDCHNLFGSYQCTCPDGYRKIGPBCVDIDECRYR	171
Qy	176	YCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPG	235
Db	172	YQHRCVNLPGSFRQCCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQG	231
Qy	236	YELEEDGVHCSMDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHR	295
Db	232	YELHRDGFSCSDIDECSSYLCQYRCVNEPGRFSCHPQGYQLL-ATRLCQDIDECESG	290
Qy	296	NHTCNLQQTCTYNLQGGFKCIDPIRCEEPYLRI SDNRMC PAENPGCRDQPFITLYRDMDV	355
Db	291	AHQCSQAQTCVNFLHGGYRCVDTNRCVBPYIQVSENRCLCPASNPLCREQPSIVHRYMTI	350
Qy	356	VSGRSVPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP	415





KW	Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.		
FT	SIGNAL	1	25
FT	CHAIN	26	443
FT	EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR		
FT	MATRIX PROTEIN 2.		
FT	DOMAIN	36	81
FT	DOMAIN	123	163
FT	DOMAIN	164	202
FT	DOMAIN	203	242
FT	DOMAIN	243	282
FT	DOMAIN	283	328
FT	DISULFID	127	140
FT	DISULFID	134	149
FT	DISULFID	151	162
FT	DISULFID	168	177
FT	DISULFID	173	186
FT	DISULFID	188	201
FT	DISULFID	207	217
FT	DISULFID	213	226
FT	DISULFID	228	241
FT	DISULFID	247	258
FT	DISULFID	254	267
FT	DISULFID	269	281
FT	DISULFID	287	300
FT	DISULFID	294	309
FT	DISULFID	315	327
FT	CARBOHYD	198	198
FT	CARBOHYD	394	394
SQ	SEQUENCE	443 AA;	49425 MW; 4969C0328A23DD88 CRC64;

Query Match 50.6%; Score 1282; DB 1; Length 443;

Best Local Similarity 49.9%; Pred. No. 5.7e-88;

Matches 226; Conservative 70; Mismatches 135; Indels 22; Gaps 4;

Qy	1	MPGIKRILTVTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG	55
		:   : :   : : :   : :   :   :   :   :   :   :	
Db	8	LPGSLLLWAFLLLLLGAASPDPEEPDSYTECTDGYEWDADSQHCRDVNECLTIPEACKG	67
Qy	56	DMMCVNQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYAPAAAPPLSAPNYPTISRPLICRF	115
		:   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	68	EMKCINHYGGYLCILPRSAAVISDLHG-----EGPPPPAA-----HAQQNPNCPO	111
Qy	116	GYQMDESNCQVDVDECATDSHQCNPTQICINTEGGYTCSDTDGYWLEGGQCLDIDECYRG	175
		:   :   :   :   :   :   :   :   :   :   :   :   :	
Db	112	GYBPDEQESQVDVDECTQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECYR	171
Qy	176	YQQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPG	235
		:   :   :   :   :   :   :   :   :   :   :   :   :	
Db	172	YQHRVCNLPGSPRCQCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCNQG	231
Qy	236	YELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSQDINECEHR	295
		:   :   :   :   :   :   :   :   :   :   :   :   :	
Db	232	YELHRDGFSCSDIDECGYSSYLQYRCVNEPGRFSCHPQGYQL-ATRLCQDIDECETG	290
Qy	296	NHTCNLQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENFGCRDQPFITYRDMV	355
		:   :   :   :   :   :   :   :   :   :   :   :   :	
Db	291	AHQCSAQTCVNPHGGYRCVDTNRCVEPIVQVSDNRCLCPASNPLCREQPSSIVHRYMSI	350

```

QY      356 VSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPKGP 415
      | |||||:|:|:|: |||| | |:| | :|:| | :| | |: | |||
Db      351 TSERSVPADVFIQATSYYPGAYNAPQIRSGNTQGDIFYIRQINNVSAMLVLAREPVTGP 410

QY      416 IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
      |||||:|:|:|: |||:| :| | |
Db      411 YVLDLEMTVMNSLMSYRASSVLRILTVPVGAYTF 443

```

# RESULT 7

## FBL3\_RAT

```

ID      FBL3_RAT          STANDARD;          PRT;          493 AA.
AC      O35568;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      EGF-containing fibulin-like extracellular matrix protein 1 precursor
DE      (Fibulin-3) (FBL-3) (T16 protein).
GN      EFEMP1 OR FBLN3.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]

```

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX MEDLINE=97415782; PubMed=9268694;

RA Ozaki T., Kondo K., Nakamura Y., Ichimiya S., Nakagawara A.,

RA Sakiyama S.;

RT "Interaction of DA41, a DAN-binding protein, with the epidermal growth

RT factor-like protein, S(1-5).";

RL Biochem. Biophys. Res. Commun. 237:245-250(1997).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the fibulin family.

CC -!- SIMILARITY: Contains 6 EGF-like domains.

-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; D89730; BAA22265.1; -.

DR PIR; JC5621; JC5621.

DR HSSP; P35555; 1EMN.

DR InterPro; IPR000152; Asx\_hydroxyl.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR006209; EGF\_like.

DR Pfam; PF00008; EGF; 3.

DR SMART; SM00179; EGF\_CA; 4.

DR PROSITE; PS00010; ASX\_HYDROXYL; 4.

DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.

DR PROSITE; PS01186; EGF\_2; 4.

DR PROSITE; PS01187; EGF\_CA; 6.

KW Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.

FT	SIGNAL	1	17	POTENTIAL.
FT	CHAIN	18	493	EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
FT				MATRIX PROTEIN 1.
FT	DOMAIN	26	71	EGF-LIKE 1, DIVERGENT.
FT	DOMAIN	173	213	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	214	253	EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	254	293	EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	294	333	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	334	378	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	DISULFID	177	190	BY SIMILARITY.
FT	DISULFID	184	199	BY SIMILARITY.
FT	DISULFID	201	212	BY SIMILARITY.
FT	DISULFID	218	228	BY SIMILARITY.
FT	DISULFID	224	237	BY SIMILARITY.
FT	DISULFID	239	252	BY SIMILARITY.
FT	DISULFID	258	268	BY SIMILARITY.
FT	DISULFID	264	277	BY SIMILARITY.
FT	DISULFID	279	292	BY SIMILARITY.
FT	DISULFID	298	309	BY SIMILARITY.
FT	DISULFID	305	318	BY SIMILARITY.
FT	DISULFID	320	332	BY SIMILARITY.
FT	DISULFID	338	350	BY SIMILARITY.
FT	DISULFID	344	359	BY SIMILARITY.
FT	DISULFID	365	377	BY SIMILARITY.
SQ	SEQUENCE	493 AA;	54596 MW;	22DAFD70BACF1CA5 CRC64;

Query Match 43.8%; Score 1109.5; DB 1; Length 493;  
 Best Local Similarity 42.3%; Pred. No. 3.8e-75;  
 Matches 206; Conservative 73; Mismatches 161; Indels 47; Gaps 5;

Qy	7	ILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGY	66
Db	9	MLTLALVKSQVTEETITYTQCTDGYEWDVPRVQCKDIDECDIVDACKGGMKCVNHYGGY	68
Qy	67	LCIPRTNPVYRGPSYNPYSTPYS-----GPYPAAAPPLSAP	102
Db	69	LCLPKTAQIIIVNNEQPQOETPAEEASSGAATGTIAARSMATSGVPIGGGFASATAVAGP	128
Qy	103	NYPT-----ISRPLICRFGYQMDENQCVDVDECATDSHCNPTQ	142
Db	129	EVQTRGRNPFVIRRNPDAPQRIPSNPSHRIQCAAGYEQSEHNVCQDIDECTSGTHNCRLDQ	188
Qy	143	ICINTEGGYTCSCTDGYWLLEGQCLDIDECRY-GYCQQLCANVPGYSYCTCNPGFTLNED	201
Db	189	VCINLRGSFTCHCLPGYQKRGEQCVDIDECVPPYCHQGCNVNTFGSFYQCQCNFGQLAAN	248
Qy	202	GRSCQDVNECATENPCVQTCVNITYGSFICRCDPGYELEDGVHCSMDDECSFSEFLCOHE	261
Db	249	NYTCVDINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEBIDBCRTSSSYLCQYQ	308
Qy	262	CVNQPGTYFCSCPPGYILLDDNRSQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCE	321
Db	309	CVNEPGKFSMCPQGYQVV-RSRTOQDINECETTNE-CREDEMCWNYHGGFRCYPQNPQ	366
Qy	322	EPYLRIISDNRCMCPAENPGCRDQPFITILYRMDVVSGRSVPADIFQMQATTRYPGAYYIF	381
Db	367	DPYVLTSENRCVCPVSNNTMCRDVPQSIYKYMNIRSDRSVPDSDFIQIQTATTIYANTINTF	426

QY 382 QIKSGNEGREFYMRQTGPISATLVMTRPPIKGPREIQLDLEMITVNTVINFRGSSVIRLRI 441  
 Db :||||| :||:| | :| | : : ||| : |||:|::| ||||| |  
 427 RIKSGNENGFEYLRTSPVSAMLVLVKSLTGPREHIVGLEMLTVSSIGTFRTSSVRLRLTI 486  
 QY 442 YVSQYPPF 448  
 Db | : |  
 487 IVGPFSF 493

RESULT 8

FBL3\_HUMAN

ID FBL3\_HUMAN STANDARD; PRT; 493 AA.  
 AC Q12805;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE EGF-containing fibulin-like extracellular matrix protein 1 precursor  
 DE (Fibulin-3) (FIBL-3) (Fibrillin-like protein) (Extracellular protein  
 DE S1-5).  
 GN EFEMP1 OR FBLN3 OR FBNL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND POSSIBLE ALTERNATIVE SPLICING.  
 RC TISSUE=Skin;  
 RX MEDLINE=95097983; PubMed=7799918;  
 RA Lecka-Czernik B., Lumpkin C.K. Jr., Goldstein S.;  
 RT "An overexpressed gene transcript in senescent and quiescent human  
 RT fibroblasts encoding a novel protein in the epidermal growth factor-  
 RT like repeat family stimulates DNA synthesis.";  
 RL Mol. Cell. Biol. 15:120-128(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97001163; PubMed=8812496;  
 RA Ikegawa S., Toda T., Okui K., Nakamura Y.;  
 RT "Structure and chromosomal assignment of the human S1-5 gene (FBNL)  
 RT that is highly homologous to fibrillin.";  
 RL Genomics 35:590-592(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20068041; PubMed=10601734;  
 RA Giltay R., Timpl R., Kostka G.;  
 RT "Sequence, recombinant expression and tissue localization of two novel  
 RT extracellular matrix proteins, fibulin-3 and fibulin-4.";  
 RL Matrix Biol. 18:469-480(1999).  
 RN [4]  
 RP VARIANT DHRD/MLVT TRP-345, AND VARIANT PHE-220.  
 RX MEDLINE=99295941; PubMed=10369267;  
 RA Stone E.M., Lotery A.J., Munier F.L., Heon E., Piguet B., Guymer R.H.,  
 RA Vandenburgh K., Cousin P., Nishimura D., Swiderski R.E., Silvestri G.,  
 RA Mackey D.A., Hagerman G.S., Bird A.C., Sheffield V.C.,  
 RA Schorderet D.F.;  
 RT "A single EFEMP1 mutation associated with both malattia Leventinese  
 RT and Doyme honeycomb retinal dystrophy.";

```

RL  Nat. Genet. 22:199-202(1999).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=4;
CC      Comment=Experimental confirmation may be lacking for some
CC      isoforms;
CC      Name=1;
CC      IsoId=Q12805-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q12805-2; Sequence=VSP_001392;
CC      Name=3;
CC      IsoId=Q12805-3; Sequence=VSP_001393;
CC      Name=4;
CC      IsoId=Q12805-4; Sequence=VSP_001394;
CC  -!- DISEASE: DEFECTS IN EFEMP1 ARE A CAUSE OF DOYNE HONEYCOMB RETINAL
CC      DYSTROPHY (DHDR) ALSO KNOWN AS MALATTIA LEVENTINESE (MLVT OR ML),
CC      AN AUTOSOMAL DOMINANT DISEASE CHARACTERIZED BY YELLOW-WHITE
CC      DEPOSITS KNOWN AS DRUSEN THAT ACCUMULATE BENEATH THE RETINAL
CC      PIGMENT EPITHELIUM.
CC  -!- SIMILARITY: Belongs to the fibulin family.
CC  -!- SIMILARITY: Contains 6 EGF-like domains.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; U03877; AAA65590.1; -.
DR  HSSP; P35555; 1EMN.
DR  Genew; HGNC:3218; EFEMP1.
DR  MIM; 601548; -.
DR  MIM; 126600; -.
DR  GO; GO:0005578; C:extracellular matrix; TAS.
DR  GO; GO:0007601; P:vision; TAS.
DR  InterPro; IPR000152; Asx_hydroxyl.
DR  InterPro; IPR001881; EGF_Ca.
DR  InterPro; IPR006209; EGF_like.
DR  Pfam; PF00008; EGF; 3.
DR  SMART; SM00179; EGF_CA; 4.
DR  PROSITE; PS00010; ASX_HYDROXYL; 4.
DR  PROSITE; PS00022; EGF_1; FALSE_NEG.
DR  PROSITE; PS01186; EGF_2; 4.
DR  PROSITE; PS01187; EGF_CA; 6.
KW  Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal;
KW  Disease mutation; Polymorphism; Alternative splicing.
FT  SIGNAL      1      17      POTENTIAL.
FT  CHAIN       18     493      EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
FT                                     MATRIX PROTEIN 1.
FT  DOMAIN      26     71      EGF-LIKE 1, DIVERGENT.
FT  DOMAIN      173    213      EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT  DOMAIN      214    253      EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT  DOMAIN      254    293      EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT  DOMAIN      294    333      EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT  DOMAIN      334    378      EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

```

FT	DISULFID	177	190	BY SIMILARITY.
FT	DISULFID	184	199	BY SIMILARITY.
FT	DISULFID	201	212	BY SIMILARITY.
FT	DISULFID	218	228	BY SIMILARITY.
FT	DISULFID	224	237	BY SIMILARITY.
FT	DISULFID	239	252	BY SIMILARITY.
FT	DISULFID	258	268	BY SIMILARITY.
FT	DISULFID	264	277	BY SIMILARITY.
FT	DISULFID	279	292	BY SIMILARITY.
FT	DISULFID	298	309	BY SIMILARITY.
FT	DISULFID	305	318	BY SIMILARITY.
FT	DISULFID	320	332	BY SIMILARITY.
FT	DISULFID	338	350	BY SIMILARITY.
FT	DISULFID	344	359	BY SIMILARITY.
FT	DISULFID	365	377	BY SIMILARITY.
FT	CARBOHYD	249	249	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	1	8	Missing (in isoform 2).
FT				/FTId=VSP_001392.
FT	VARSPLIC	58	58	Missing (in isoform 3).
FT				/FTId=VSP_001393.
FT	VARSPLIC	106	106	Missing (in isoform 4).
FT				/FTId=VSP_001394.
FT	VARIANT	220	220	I -> F.
FT				/FTId=VAR_009512.
FT	VARIANT	345	345	R -> W (IN MVLT).
FT				/FTId=VAR_009513.
SQ	SEQUENCE	493 AA;	54640 MW;	128CASED140DF414 CRC64;

QY		6	RILTVTIIALCLPSPGNAQ----	AQCTNGFDLDRQSGQCGLDIDECRTIPEACRGDMMCV	60
			:   :   :   :   :   :   :   :   :   :   :   :   :   :		
Db		3	KALFLTMLTLALVKSQDTREETITYTQCTDGYEWDPVRRQQCKDIDECDIVPDAKGGMKCV	62	
QY		61	NQNGGYYLCIPRTNPVY-----RGPYSNPY-----STPYSGPYPA-----	95	
			:   :   :   :   :   :   :   :   :   :   :		
Db		63	NHYGGYLCLEPKTAQIIVNNEQPQEQTPAEGTSGATTGVVAASSMATSGVLPGGGFVASA	122	
QY		96	-----APPLSAPNYPTISRPLICRFGYQMDESNCVDVDECATD	134	
			:   :   :   :   :   :   :   :   :   :   :		
Db		123	AAVAGPEMQTRNNFVIRRNPADQRIFSNP--SHRIQCAAGYEQSEHNVCQDIDECTAG	180	
QY		135	SHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCGLDIDECRY-GYCQQLCANVPGSYSTCN	193	
			:   :   :   :   :   :   :   :   :   :   :		
Db		181	THNCRADQVCINLRGSFAQCPCPPGYQKRGEQCDVIDECTIPPYCHQRCVNTPGFSFYCQS	240	
QY		194	PGFTLNEDGRSCQDVNECATENPCVQTVMNTYGSFICRCPDGYELEEDBGVHCSDMDECSF	253	
			:   :   :   :   :   :   :   :   :   :   :   :		
Db		241	PGFQLAANNNTCVDINECDASNQCAQQCYNILGSFICQNQGYELSSDRLNCEBIDECRT	300	
QY		254	SEFLCQHECVNQGPTYFCSCP PGYILLDDNRNSQCDINECEHRNHNTCNLQQTCCYNLQGGFK	313	
			:   :   :   :   :   :   :   :   :   :   :   :		
Db		301	SSYLCCQYQCVNEFGKFSCMPQGYQVV-RRSTQCDINECETTNE-CREDEMCCWNHGGFR	358	
QY		314	CIDPIRCBEPLYRLISDNRMCMCPAENPGCRDPFTILYRDMDVVSGRSVPADIFQMQAATTR	373	

Db 359 |::|: :||:| | |::| :|:|: | : | |||:|::|:| |  
 CYPNPCQDPYILTPENRCVCPVSNAMCRELPQSIVYKMSIRSDRSVPSDIPQIATTI 418  
 QY 374 YPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRG 433  
 | :|:|:| | |::|:| |::| |: : : | | | :|:|:|:|:|:| |  
 Db 419 YANTINTPRIKSGNENGEFYLRQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFT 478  
 QY 434 SSVIRLRIYVSQYPF 448  
 |::|:| | : |  
 Db 479 SSVRLRTIIVGPFPSF 493

# RESULT 9

## FBL2\_MOUSE

ID FBL2\_MOUSE STANDARD; PRT; 1221 AA.  
 AC P37889; Q9WUI2;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Fibulin-2 precursor.  
 GN FBLN2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-35.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=94064787; PubMed=8245130;  
 RA Pan T.-C., Sasaki T., Zhang R.-Z., Faessler R., Timpl R., Chu M.-L.;  
 RT "Structure and expression of fibulin-2, a novel extracellular matrix  
 RT protein with multiple EGF-like repeats and consensus motifs for  
 RT calcium binding."  
 RL J. Cell Biol. 123:1269-1277(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RX MEDLINE=99337686; PubMed=10406956;  
 RA Graessel S., Sicot F.-X., Gotta S., Chu M.-L.;  
 RT "Mouse fibulin-2 gene. Complete exon-intron organization and promoter  
 RT characterization."  
 RL Eur. J. Biochem. 263:471-477(1999).  
 RN [3]  
 RP DEVELOPMENTAL STAGE.  
 RX PubMed=8850569;  
 RA Zhang H.-Y., Timpl R., Sasaki T., Chu M.-L., Ekblom P.;  
 RT "Fibulin-1 and fibulin-2 expression during organogenesis in the  
 RT developing mouse embryo."  
 RL Dev. Dyn. 205:348-364(1996).  
 RN [4]  
 RP BINDING TO LAMA2.  
 RX PubMed=10022829;  
 RA Talts J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;  
 RT "Binding of the G domains of laminin alpha1 and alpha2 chains and  
 RT perlecan to heparin, sulfatides, alpha-dystroglycan and several  
 RT extracellular matrix proteins."  
 RL EMBO J. 18:863-870(1999).  
 RN [5]



RP DOWN-REGULATION BY GLUCOCORTICOIDS.  
RX PubMed=11737251;  
RA Gu Y.-C., Talts J.F., Gullberg D., Timpl R., Ekblom M.;  
RT "Glucocorticoids down-regulate the extracellular matrix proteins  
RT fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";  
RL Eur. J. Haematol. 67:176-184(2001).  
CC -!- FUNCTION: ITS BINDING TO FIBRONECTIN AND SOME OTHER LIGANDS IS  
CC CALCIUM DEPENDENT.  
CC -!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2.  
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Comment=Additional isoforms seem to exist;  
CC Name=1;  
CC IsoId=P37889-1; Sequence=Displayed;  
CC Name=2; Synonyms=EGF3-less;  
CC IsoId=P37889-2; Sequence=VSP\_001391;  
CC -!- TISSUE SPECIFICITY: Component of both basement membranes and other  
CC connective tissues.  
CC -!- DEVELOPMENTAL STAGE: The differential expression of the fibulin  
CC family contributes to the formation of molecularly distinct  
CC extracellular matrices already during early developmental stages  
CC of a large number of tissues.  
CC -!- INDUCTION: Glucocorticoids suppressed mRNA expression and protein  
CC synthesis.  
CC -!- SIMILARITY: Belongs to the fibulin family.  
CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.  
CC -!- SIMILARITY: Contains 11 EGF-like domains.

-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; X75285; CAA53040.1; -.  
DR EMBL; AF135253; AAD34456.1; -.  
DR EMBL; AF135239; AAD34456.1; JOINED.  
DR EMBL; AF135240; AAD34456.1; JOINED.  
DR EMBL; AF135241; AAD34456.1; JOINED.  
DR EMBL; AF135242; AAD34456.1; JOINED.  
DR EMBL; AF135243; AAD34456.1; JOINED.  
DR EMBL; AF135244; AAD34456.1; JOINED.  
DR EMBL; AF135245; AAD34456.1; JOINED.  
DR EMBL; AF135246; AAD34456.1; JOINED.  
DR EMBL; AF135247; AAD34456.1; JOINED.  
DR EMBL; AF135248; AAD34456.1; JOINED.  
DR EMBL; AF135249; AAD34456.1; JOINED.  
DR EMBL; AF135250; AAD34456.1; JOINED.  
DR EMBL; AF135251; AAD34456.1; JOINED.  
DR EMBL; AF135252; AAD34456.1; JOINED.  
DR PIR; A49457; A49457.  
DR HSSP; P00736; 1APQ.  
DR MGD; MGI:95488; Fbln2.  
DR InterPro; IPR000020; Anaphylatoxin.

DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR Pfam; PF01821; ANATO; 2.  
 DR Pfam; PF00008; EGF; 6.  
 DR SMART; SM00104; ANATO; 3.  
 DR SMART; SM00179; EGF\_CA; 9.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 5.  
 DR PROSITE; PS01177; ANAPHYLATOXIN\_1; 3.  
 DR PROSITE; PS01178; ANAPHYLATOXIN\_2; 3.  
 DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE; PS01186; EGF\_2; 5.  
 DR PROSITE; PS01187; EGF\_CA; 10.  
 KW Signal; Glycoprotein; Extracellular matrix; Plasma; EGF-like domain;  
 KW Calcium-binding; Alternative splicing; Repeat.  
 FT SIGNAL 1 26  
 FT CHAIN 27 1221 FIBULIN-2.  
 FT DOMAIN 27 434 N.  
 FT DOMAIN 27 176 SUBDOMAIN NA (CYS-RICH).  
 FT DOMAIN 177 434 SUBDOMAIN NB (CYS-FREE).  
 FT DOMAIN 435 477 ANAPHYLATOXIN-LIKE 1.  
 FT DOMAIN 478 510 ANAPHYLATOXIN-LIKE 2.  
 FT DOMAIN 511 543 ANAPHYLATOXIN-LIKE 3.  
 FT DOMAIN 594 635 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 669 708 EGF-LIKE 2.  
 FT DOMAIN 709 755 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 756 800 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 801 846 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 847 894 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 895 937 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 938 979 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 980 1018 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 1019 1061 EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 1062 1106 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 1111 1221 DOMAIN III.  
 FT SITE 421 423 CELL ATTACHMENT SITE (POTENTIAL).  
 FT DISULFID 435 462 BY SIMILARITY.  
 FT DISULFID 436 469 BY SIMILARITY.  
 FT DISULFID 449 470 BY SIMILARITY.  
 FT DISULFID 479 508 BY SIMILARITY.  
 FT DISULFID 492 509 BY SIMILARITY.  
 FT DISULFID 511 535 BY SIMILARITY.  
 FT DISULFID 512 542 BY SIMILARITY.  
 FT DISULFID 525 543 BY SIMILARITY.  
 FT DISULFID 598 610 BY SIMILARITY.  
 FT DISULFID 606 619 BY SIMILARITY.  
 FT DISULFID 621 634 BY SIMILARITY.  
 FT DISULFID 673 683 BY SIMILARITY.  
 FT DISULFID 679 692 BY SIMILARITY.  
 FT DISULFID 694 707 BY SIMILARITY.  
 FT DISULFID 713 726 BY SIMILARITY.  
 FT DISULFID 720 735 BY SIMILARITY.  
 FT DISULFID 742 754 BY SIMILARITY.  
 FT DISULFID 805 818 BY SIMILARITY.  
 FT DISULFID 812 827 BY SIMILARITY.  
 FT DISULFID 833 845 BY SIMILARITY.  
 FT DISULFID 899 912 BY SIMILARITY.

FT	DISULFID	906	921	BY SIMILARITY.
FT	DISULFID	923	936	BY SIMILARITY.
FT	DISULFID	942	954	BY SIMILARITY.
FT	DISULFID	950	963	BY SIMILARITY.
FT	DISULFID	965	978	BY SIMILARITY.
FT	DISULFID	984	993	BY SIMILARITY.
FT	DISULFID	989	1002	BY SIMILARITY.
FT	DISULFID	1004	1017	BY SIMILARITY.
FT	DISULFID	1023	1035	BY SIMILARITY.
FT	DISULFID	1031	1044	BY SIMILARITY.
FT	DISULFID	1046	1060	BY SIMILARITY.
FT	DISULFID	1066	1079	BY SIMILARITY.
FT	DISULFID	1073	1088	BY SIMILARITY.
FT	DISULFID	1093	1105	BY SIMILARITY.
FT	CARBOHYD	179	179	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	497	497	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	737	737	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1072	1072	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	709	755	Missing (in isoform 2).
FT				/FTid=VSP_001391.
FT	CONFLICT	140	159	HSGRKYAAGHTVHLSSCRAC -> TVAVSICWPYRPPLILP
FT				GF (IN REF. 2).
FT	CONFLICT	348	348	S -> L (IN REF. 2).
FT	CONFLICT	507	507	Q -> QQ (IN REF. 2).
FT	CONFLICT	1102	1102	Q -> E (IN REF. 2).
SQ	SEQUENCE	1221 AA;	131818 MW;	87DB2A10A8FDC45F CRC64;

Query Match 29.0%; Score 733.5; DB 1; Length 1221;  
 Best Local Similarity 35.3%; Pred. No. 6.3e-47;  
 Matches 146; Conservative 60; Mismatches 149; Indels 59; Gaps 11;

Qy	23	AQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDDMMCVNQNGGYLCIPRTNPNVYRGPYSN	82
Db	829	ARQRCMDGF-LQDPEGNCVDINBCTSLLEPCRSRGFSCINTVGSYTC-----	873
Qy	83	PYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDCECATDSHCNQNT	141
Db	874	-----QRNPLVCGRGYHANEEGSECVDVNECETGVHRCGEG	909
Qy	142	QICINTEGGYTCSTCTDGYW--LLEGQCLDIDECRYG--YCQQLCANVPGSYSCTCNPGF	196
Db	910	QLCYNLPGSYRCDCCKPGFQRDAFGRTCIDVNBECWVSPGRLQCHTCENTPGSYRCSCAAGF	969
Qy	197	TLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELBEDGVHCSMDDECS-FSE	255
Db	970	LLAADGKHCEDVNBCESTR--CSQBCANIYGSYQCYCRQGYQLABDGHCTCTDIDECAGGAG	1028
Qy	256	FLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCTYNLQGGFKC	314
Db	1029	ILCTFRCVNPGSVQCACPBQGYTMMANGRSCKDLDECALGTHNCSEATCHNIQGSFRC	1088
Qy	315	IDPIRCEEPLYLRISDNRCMCPAENPGCRD-----QPPTILYRDMDVVSGRSVPADIFQM	368
Db	1089	L-RFDCPNYVRVSQTKC---ERTTCQDITECQTSAPARITHYQLNFQTLGLVPAHIFRI	1143
Qy	369	QATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRIPIKGPREIQLDLEM	422

## RESULT 10

## FBL1\_CERAE

ID FBL1\_CERAE STANDARD; PRT; 598 AA.  
AC Q8MJJ9;  
DT 15-SEP-2003 (Rel. 42, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Fibulin-1C (Fragment).  
GN FBLN1.  
OS Cercopithecus aethiops (Green monkey) (Grivet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]  
RP SEQUENCE FROM N.A., AND INTERACTION WITH DTR.  
RX PubMed=11846885;  
RA Brooke J.S., Cha J.-H., Eidels L.;  
RT "Latent transforming growth factor beta-binding protein-3 and  
RT fibulin-1C interact with the extracellular domain of the  
RT heparin-binding EGF-like growth factor precursor.";  
RL BMC Cell Biol. 3:2-2(2002).  
CC -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.  
CC May play a role in cell adhesion and migration along protein  
CC fibers within the extracellular matrix (ECM). Could be important  
CC for certain developmental processes and contribute to the  
CC supramolecular organization of ECM architecture, in particular to  
CC those of basement membranes. May serve to anchor the  
CC mature/soluble form of DTR to its fibers as it migrates through  
CC the extracellular matrix. The direct physical association with DTR  
CC may be useful in such tissue developmental processes as wound  
CC healing.  
CC -!- SUBUNIT: Interacts with itself and with various extracellular  
CC matrix components (By similarity). Interacts with the  
CC mature/soluble form of DTR.  
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.  
CC -!- SIMILARITY: Belongs to the fibulin family.  
CC -!- SIMILARITY: Contains at least 2 anaphylatoxin-like domains.  
CC -!- SIMILARITY: Contains 9 EGF-like domains.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF395659; AAM90567.1; -.  
DR InterPro; IPR000020; Anaphylatoxin.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR006210; IEGF.

DR	Pfam; PF01821; ANATO; 1.		
DR	Pfam; PF00008; EGF; 5.		
DR	SMART; SM00104; ANATO; 1.		
DR	SMART; SM00181; EGF; 9.		
DR	SMART; SM00179; EGF_CA; 9.		
DR	PROSITE; PS01177; ANAPHYLATOXIN_1; 1.		
DR	PROSITE; PS01178; ANAPHYLATOXIN_2; 1.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 4.		
DR	PROSITE; PS01186; EGF_2; 3.		
DR	PROSITE; PS01187; EGF_CA; 7.		
KW	Glycoprotein; Extracellular matrix; Repeat; EGF-like domain;		
KW	Calcium-binding.		
FT	NON_TER	1	
FT	CHAIN	<1	598 FIBULIN-1C.
FT	DOMAIN	<1	27 ANAPHYLATOXIN-LIKE 2.
FT	DOMAIN	28	60 ANAPHYLATOXIN-LIKE 3.
FT	DOMAIN	92	131 EGF-LIKE 1.
FT	DOMAIN	132	177 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	178	223 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	224	270 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	271	313 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	314	355 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	356	395 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	396	439 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	440	484 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	271	355 SELF-ASSOCIATION AND FN1-BINDING (BY SIMILARITY).
FT	DISULFID	<1	25 BY SIMILARITY.
FT	DISULFID	7	26 BY SIMILARITY.
FT	DISULFID	28	52 BY SIMILARITY.
FT	DISULFID	29	59 BY SIMILARITY.
FT	DISULFID	42	60 BY SIMILARITY.
FT	DISULFID	96	106 BY SIMILARITY.
FT	DISULFID	102	115 BY SIMILARITY.
FT	DISULFID	117	130 BY SIMILARITY.
FT	DISULFID	136	149 BY SIMILARITY.
FT	DISULFID	143	158 BY SIMILARITY.
FT	DISULFID	164	176 BY SIMILARITY.
FT	DISULFID	182	195 BY SIMILARITY.
FT	DISULFID	189	204 BY SIMILARITY.
FT	DISULFID	210	222 BY SIMILARITY.
FT	DISULFID	228	242 BY SIMILARITY.
FT	DISULFID	257	270 BY SIMILARITY.
FT	DISULFID	275	288 BY SIMILARITY.
FT	DISULFID	282	297 BY SIMILARITY.
FT	DISULFID	299	312 BY SIMILARITY.
FT	DISULFID	318	330 BY SIMILARITY.
FT	DISULFID	326	339 BY SIMILARITY.
FT	DISULFID	341	354 BY SIMILARITY.
FT	DISULFID	360	369 BY SIMILARITY.
FT	DISULFID	365	378 BY SIMILARITY.
FT	DISULFID	380	394 BY SIMILARITY.
FT	DISULFID	400	413 BY SIMILARITY.
FT	DISULFID	409	422 BY SIMILARITY.
FT	DISULFID	424	438 BY SIMILARITY.
FT	DISULFID	444	457 BY SIMILARITY.
FT	DISULFID	451	466 BY SIMILARITY.

FT DISULFID 471 483 BY SIMILARITY.  
 FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 598 AA; 65516 MW; 849BF018DF452B02 CRC64;

Query Match 28.7%; Score 728; DB 1; Length 598;  
 Best Local Similarity 34.8%; Pred. No. 8e-47;  
 Matches 158; Conservative 76; Mismatches 188; Indels 32; Gaps 16;

```

Qy      16 CLPSPGNAQAQ---CTNGFDLDRQSGQCLDIDECDRTIPEACRGMCMCVNQNGGYLCIPR 71
      | : : : : | | : : | : : | : : | : : | : : | : : | : : | : :
Db      149 CINTVGSRFCQRDSSCGTYGEL-TEDNSCKDIDQCESGIHNCLPDFICQNTLGSFRCRPK 207

Qy      72 ---TNPVYRGYPYSNYS-----TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESN 123
      | : : : | : : | : : | : : | : : | : : | : : | : : | : :
Db      208 LQCKNGFIQDALANCIDINECLSIVSAPCPTGHTCINTEGYSYTKQNVNPGCRGYHLNEEG 267

Qy      124 QCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQ 178
      | : : : | : : | : : | : : | : : | : : | : : | : : | : :
Db      268 TRCDVNECAPPAEPCEGKHCNVNPGSFRCECKTGYYPDGISRMCDVNECQRYPGRLCG 327

Qy      179 QLCANVPGSYSCTCNPGFTLNEGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYEL 238
      | | | | | : : | : | : | : | : | : | : | : | : | : | : | :
Db      328 HKCENTLGSYVCSVSGFRLSVDGSRCEIDINECSS-SPCSQECANVYGSYQCYCRRGYQL 386

Qy      239 EE-DGVHCSMDMECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEH 294
      : | : | | : : | : : | : : | : : | : : | : : | : : | : : | : :
Db      387 SDVDGVTCEIDICALPTGGHICSYRCINIPGSFQCSCPASGYRLAPNGRNQCQDIDECVT 446

Qy      295 RNHTCNLQQTCTYNLQGGFKCIDPIRCEEPLYRLISDNRC-MCPA-ENPGCRDQPFTILYRD 352
      | : : : | : : | : : | : : | : : | : : | : : | : : | : :
Db      447 GIHNCSINETCFNIQGGFRCL-AFECPENYRRSAATRCERLPCHENRECSKPLRITYYH 505

Qy      353 MDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTPISATLVMTRPIKG 412
      : : : | : : | : : | : : | : : | : : | : : | : : | : :
Db      506 LSFPTNIQAPAVVFRMGPSAVPGDSMQLAITGGNEEGFTTRKVSFHSQGVVALTKPVPE 565

Qy      413 PREIQLDLEM--ITVNTVINFRGSSVIRLRIYVS 444
      | : : | : : | : : | : : | : : | : : | : : | : :
Db      566 PRDLLLTVMKMDLYRHGTVSSF----VAKLFIFVS 595
  
```

# RESULT 11

## FBL1\_CHICK

ID FBL1\_CHICK STANDARD; PRT; 704 AA.  
 AC 073775; 073774;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Fibulin-1 precursor.  
 GN FBLN1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;

RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS C AND D).  
 RC TISSUE=Embryo;  
 RX MEDLINE=99120531; PubMed=9923656;  
 RA Barth J.L., Argraves K.M., Roark E.F., Little C.D., Argraves W.S.;  
 RT "Identification of chicken and C. elegans fibulin-1 homologs and  
 RT characterization of the C. elegans fibulin-1 gene.";  
 RL Matrix Biol. 17:635-646(1998).  
 CC -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.  
 CC May play a role in cell adhesion and migration along protein  
 CC fibers within the extracellular matrix (ECM). Could be important  
 CC for certain developmental processes and contribute to the  
 CC supramolecular organization of ECM architecture, in particular to  
 CC those of basement membranes.  
 CC -!- SUBUNIT: Interacts with itself and with various extracellular  
 CC matrix components (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=D;  
 CC IsoId=073775-2; Sequence=Displayed;  
 CC Name=C;  
 CC IsoId=073775-1; Sequence=VSP\_007378;  
 CC -!- SIMILARITY: Belongs to the fibulin family.  
 CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.  
 CC -!- SIMILARITY: Contains 9 EGF-like domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF051399; AAC05387.1; -.  
 DR EMBL; AF051400; AAC05388.1; -.  
 DR HSP; P00742; 1HCG.  
 DR InterPro; IPR000020; Anaphylatoxin.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR Pfam; PF01821; ANATO; 2.  
 DR Pfam; PF00008; EGF; 6.  
 DR SMART; SM00104; ANATO; 3.  
 DR SMART; SM00181; EGF; 9.  
 DR SMART; SM00179; EGF\_CA; 8.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 5.  
 DR PROSITE; PS01177; ANAPHYLATOXIN\_1; 1.  
 DR PROSITE; PS01178; ANAPHYLATOXIN\_2; 2.  
 DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_CA; 8.  
 KW Signal; Alternative splicing; Glycoprotein; Extracellular matrix;  
 KW Repeat; EGF-like domain; Calcium-binding.  
 FT SIGNAL 1 25 POTENTIAL.  
 FT CHAIN 26 704 FIBULIN-1.

FT	DOMAIN	33	74	ANAPHYLATOXIN-LIKE 1.
FT	DOMAIN	75	109	ANAPHYLATOXIN-LIKE 2.
FT	DOMAIN	110	142	ANAPHYLATOXIN-LIKE 3.
FT	DOMAIN	177	216	EGF-LIKE 1.
FT	DOMAIN	217	262	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	263	308	EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	309	356	EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	357	399	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	400	441	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	442	481	EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	482	525	EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	526	579	EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	357	441	SELF-ASSOCIATION AND FN1-BINDING (BY
FT				SIMILARITY).
FT	DISULFID	33	59	BY SIMILARITY.
FT	DISULFID	34	66	BY SIMILARITY.
FT	DISULFID	47	67	BY SIMILARITY.
FT	DISULFID	76	107	BY SIMILARITY.
FT	DISULFID	89	108	BY SIMILARITY.
FT	DISULFID	110	134	BY SIMILARITY.
FT	DISULFID	111	141	BY SIMILARITY.
FT	DISULFID	124	142	BY SIMILARITY.
FT	DISULFID	181	191	BY SIMILARITY.
FT	DISULFID	187	200	BY SIMILARITY.
FT	DISULFID	202	215	BY SIMILARITY.
FT	DISULFID	221	234	BY SIMILARITY.
FT	DISULFID	228	243	BY SIMILARITY.
FT	DISULFID	249	261	BY SIMILARITY.
FT	DISULFID	267	280	BY SIMILARITY.
FT	DISULFID	274	289	BY SIMILARITY.
FT	DISULFID	295	307	BY SIMILARITY.
FT	DISULFID	313	326	BY SIMILARITY.
FT	DISULFID	320	335	BY SIMILARITY.
FT	DISULFID	342	355	BY SIMILARITY.
FT	DISULFID	361	374	BY SIMILARITY.
FT	DISULFID	368	383	BY SIMILARITY.
FT	DISULFID	385	398	BY SIMILARITY.
FT	DISULFID	404	416	BY SIMILARITY.
FT	DISULFID	412	425	BY SIMILARITY.
FT	DISULFID	427	440	BY SIMILARITY.
FT	DISULFID	446	455	BY SIMILARITY.
FT	DISULFID	451	464	BY SIMILARITY.
FT	DISULFID	466	480	BY SIMILARITY.
FT	DISULFID	486	499	BY SIMILARITY.
FT	DISULFID	495	508	BY SIMILARITY.
FT	DISULFID	510	524	BY SIMILARITY.
FT	DISULFID	530	543	BY SIMILARITY.
FT	DISULFID	537	552	BY SIMILARITY.
FT	DISULFID	557	578	BY SIMILARITY.
FT	CARBOHYD	96	96	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	536	536	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	540	540	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSP LIC	568	704	VRLEKTDITRICTKSCRPNVNCVLDPVHTISHTVISLPTFR
FT				EFTRP EEIIFLRAITPTYPANQADIIFDITEGNLRESFDII
FT				KRYMDGMTGVGVQRPIVGPFFHAILKLEMNVMGGVVS HR
FT				NIVNVHIFVSEYWF -> RCERLPCNENKECQSLPLRITYY
FT				HLSPPTNIQVPTDIFRMGPSNAVPGDKILLSISGNQBQFF



```

FT                                     TTKKVNHHSGIVVMQRQITEPRDLLLTIQMLTRHGTVMTF
FT                                     IAKLFVVFVSAQL (in isoform C).
FT                                     /FTId=VSP_007378.
SO    SEQUENCE      704 AA;  78137 MW;  D47D5A30D5E42932 CRC64;

```

Qy	15	LCLPSPGN---AAQAQCTMGFDLDRQSQQLDIDECRTIPEACRGDMMCVNQNGGYLCIP	70
Db	279	ICQNTPGSFRRCRPKLQCMNGFIQD-ALGNCIDINECLSTNMPCPAGQICINTDGSYTC-Q	336
Qy	71	RTNPVYRGPSNPYSTPYSGPYAAAPLSAPNYPTISRPLICRFGYQMDSE-SNQCVDVD	129
Db	337	RISP-----SCGRGYHLNEDGTGRCVDVD	359
Qy	130	ECATDSHQCNPTQICINTEGGYTCSDTDGYW--LLEGQQLDIDECRY---GYCQQLCANV	184
Db	360	ECSSSDQPCGEGHVCIINGPGNYRCECKSGYSPDVISRTCIDINECRYPGRGLCAHKCENT	419
Qy	185	PGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGV	243
Db	420	PGSYICTCTMGFKLSSDGRSCEDLNECES-SPCSQBCANVYGSYQCYCRRGFLQSLDIDGI	478
Qy	244	HCSMDMECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCN	300
Db	479	SCEDIDECALPTGGHICSFRCINIPGSFQCTCPSTGYRLAPNARNCQDIDECVAETHNCS	538
Qy	301	LQQTCTYNLQGGFKCIDPIRCEEPYLRISDN-----RCM--CPAENPGC-RDQPFTI	348
Db	539	PNETCFNIQGGPRCLS-LECPENYRKSGDTVRLEKTDITRCIKSCRPNVDNVCVLDPVHTI	597
Qy	349	LYRDMDVVSGRSV--PADIFQMQA-TTRYPG--AYYIFQIKSGNEGREF----YMRQTG	398
Db	598	SHTVISLPTFPREPTRPEEIIFLRAITPTYPAQADIIFDITEGNLRESFDIIKRYM--DG	655
Qy	399	PISATLVMTRPIKGPRIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF	448
Db	656	MTVGVVROVRPIVGFPHAILKLENNYMGGVVSHR--NIVNVHIVSVSYWF	704

FBL2 HUMAN

RC TISSUE=Fibroblast;  
 RX MEDLINE=95104855; PubMed=7806230;  
 RA Zhang R.-Z., Pan T.-C., Zhang Z.-Y., Mattei M.-G., Timpl R.,  
 RA Chu M.-L.;  
 RT "Fibulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping  
 RT of the gene on human and mouse chromosomes.";  
 RL Genomics 22:425-430(1994).  
 RN [2]  
 RP DEVELOPMENTAL STAGE.  
 RX PubMed=8737292;  
 RA Miosge N., Gotz W., Sasaki T., Chu M.-L., Timpl R., Herken R.;  
 RT "The extracellular matrix proteins fibulin-1 and fibulin-2 in the  
 RT early human embryo.";  
 RL Histochem. J. 28:109-116(1996).  
 CC -!- FUNCTION: ITS BINDING TO FIBRONECTIN AND SOME OTHER LIGANDS IS  
 CC CALCIUM DEPENDENT.  
 CC -!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2 (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.  
 CC -!- TISSUE SPECIFICITY: Component of both basement membranes and other  
 CC connective tissues. Expressed in heart, placenta and ovary.  
 CC -!- DEVELOPMENTAL STAGE: Widely expressed during embryonic  
 CC development. Primarily detected within the neuroepithelium, spinal  
 CC ganglia and peripheral nerves.  
 CC -!- SIMILARITY: Belongs to the fibulin family.  
 CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.  
 CC -!- SIMILARITY: Contains 11 EGF-like domains.

-----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL; X82494; CAA57876.1; -.  
 DR PIR; A55184; A55184.  
 DR HSSP; P00736; 1APQ.  
 DR Genew; HGNC:3601; FBLN2.  
 DR MIM; 135821; -.  
 DR GO; GO:0005578; C:extracellular matrix; TAS.  
 DR GO; GO:0005509; F:calcium ion binding activity; TAS.  
 DR GO; GO:0005207; F:extracellular matrix glycoprotein; TAS.  
 DR InterPro; IPR000020; Anaphylatoxin.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR Pfam; PF01821; ANATO; 2.  
 DR Pfam; PF00008; EGF; 7.  
 DR SMART; SM00104; ANATO; 3.  
 DR SMART; SM00179; EGF\_Ca; 9.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 5.  
 DR PROSITE; PS01177; ANAPHYLATOXIN\_1; 3.  
 DR PROSITE; PS01178; ANAPHYLATOXIN\_2; 3.  
 DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE; PS01186; EGF\_2; 5.

PROSITE; PS01187; EGF_CA; 9.		
KW	Signal; Glycoprotein; Extracellular matrix; Plasma; EGF-like domain;	
KW	Calcium-binding; Repeat.	
FT	SIGNAL	1 27 POTENTIAL.
FT	CHAIN	28 1184 FIBULIN-2.
FT	DOMAIN	28 444 N.
FT	DOMAIN	28 177 SUBDOMAIN NA (CYS-RICH).
FT	DOMAIN	178 444 SUBDOMAIN NB (CYS-FREE).
FT	DOMAIN	445 480 ANAPHYLATOXIN-LIKE 1.
FT	DOMAIN	488 519 ANAPHYLATOXIN-LIKE 2.
FT	DOMAIN	521 553 ANAPHYLATOXIN-LIKE 3.
FT	DOMAIN	604 645 EGF-LIKE 1, CALCIUM-BINDING.
FT	DOMAIN	679 718 EGF-LIKE 2.
FT	DOMAIN	719 763 EGF-LIKE 3, CALCIUM-BINDING.
FT	DOMAIN	764 809 EGF-LIKE 4, CALCIUM-BINDING.
FT	DOMAIN	810 857 EGF-LIKE 5, CALCIUM-BINDING.
FT	DOMAIN	858 900 EGF-LIKE 6, CALCIUM-BINDING.
FT	DOMAIN	901 942 EGF-LIKE 7, CALCIUM-BINDING.
FT	DOMAIN	943 981 EGF-LIKE 8, CALCIUM-BINDING.
FT	DOMAIN	982 1024 EGF-LIKE 9, CALCIUM-BINDING.
FT	DOMAIN	1025 1069 EGF-LIKE 10, CALCIUM-BINDING.
FT	DOMAIN	1070 1184 DOMAIN III.
FT	DISULFID	445 472 BY SIMILARITY.
FT	DISULFID	446 479 BY SIMILARITY.
FT	DISULFID	459 480 BY SIMILARITY.
FT	DISULFID	489 518 BY SIMILARITY.
FT	DISULFID	502 519 BY SIMILARITY.
FT	DISULFID	521 545 BY SIMILARITY.
FT	DISULFID	522 552 BY SIMILARITY.
FT	DISULFID	535 553 BY SIMILARITY.
FT	DISULFID	608 620 BY SIMILARITY.
FT	DISULFID	616 629 BY SIMILARITY.
FT	DISULFID	631 644 BY SIMILARITY.
FT	DISULFID	683 693 BY SIMILARITY.
FT	DISULFID	689 702 BY SIMILARITY.
FT	DISULFID	704 717 BY SIMILARITY.
FT	DISULFID	723 736 BY SIMILARITY.
FT	DISULFID	730 745 BY SIMILARITY.
FT	DISULFID	751 762 BY SIMILARITY.
FT	DISULFID	768 781 BY SIMILARITY.
FT	DISULFID	775 790 BY SIMILARITY.
FT	DISULFID	796 808 BY SIMILARITY.
FT	DISULFID	814 827 BY SIMILARITY.
FT	DISULFID	821 836 BY SIMILARITY.
FT	DISULFID	843 856 BY SIMILARITY.
FT	DISULFID	862 875 BY SIMILARITY.
FT	DISULFID	869 884 BY SIMILARITY.
FT	DISULFID	886 899 BY SIMILARITY.
FT	DISULFID	905 917 BY SIMILARITY.
FT	DISULFID	913 926 BY SIMILARITY.
FT	DISULFID	928 941 BY SIMILARITY.
FT	DISULFID	947 956 BY SIMILARITY.
FT	DISULFID	952 965 BY SIMILARITY.
FT	DISULFID	967 980 BY SIMILARITY.
FT	DISULFID	986 998 BY SIMILARITY.
FT	DISULFID	994 1007 BY SIMILARITY.
FT	DISULFID	1009 1023 BY SIMILARITY.

Query Match 28.0%; Score 709.5; DB 1; Length 1184;  
Best Local Similarity 34.3%; Pred. No. 3.7e-45;  
Matches 146; Conservative 61; Mismatches 156; Indels 63; Gaps 12;

```

RESULT 13
FBL1_HUMAN
ID   FBL1_HUMAN          STANDARD;          PRT;       703 AA.
AC   P23142; P23143; P23144; P37888; Q8TBH8; Q9HBQ5; Q9UGR4; Q9UH41;
DT   01-NOV-1991 (Rel. 20, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Fibulin-1 precursor.
GN   FBLN1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).  
 RX MEDLINE=91100426; PubMed=2269669;  
 RA Argraves W.S., Tran H., Burgess W.H., Dickerson K.;  
 RT "Fibulin is an extracellular matrix and plasma glycoprotein with  
 RT repeated domain structure.";  
 RL J. Cell Biol. 111:3155-3164(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM D), TISSUE SPECIFICITY, AND INTERACTION  
 RP WITH FN1 AND FGB.  
 RX PubMed=9106159;  
 RA Tran H., Mattei M., Godyna S., Argraves W.S.;  
 RT "Human fibulin-1D: molecular cloning, expression and similarity with  
 RT S1-5 protein, a new member of the fibulin gene family.";  
 RL Matrix Biol. 15:479-493(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM D).  
 RX MEDLINE=99253993; PubMed=10318851;  
 RA Krichevsky A.M., Metzger E., Rosen H.;  
 RT "Translational control of specific genes during differentiation of  
 RT HL-60 cells.";  
 RL J. Biol. Chem. 274:14295-14305(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM C).  
 RA Gu J.R., Wan D.P., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,  
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
 RA Yu J., Han L.H.;  
 RT "Novel Human cDNA clones with function of inhibiting cancer cell  
 RT growth.";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20057165; PubMed=10591208;  
 RA Dunham I., Hunt A.R., Collins J.E., Bruskiwich R., Beare D.M.,  
 RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,  
 RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,  
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,  
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,  
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,  
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,  
 RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,  
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,  
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,  
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,  
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,  
 RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,  
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,  
 RA McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,  
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,  
 RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,  
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,  
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,  
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,  
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,  
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,

RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,  
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,  
 RA Dorman A., Pang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Mala J. E., Nguyen T., Pan H.,  
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,  
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,  
 RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,  
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,  
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,  
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,  
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,  
 RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,  
 RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,  
 RA Dermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,  
 RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,  
 RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,  
 RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,  
 RA Tilahun Y., Wright H.;  
 RT "The DNA sequence of human chromosome 22.";  
 RL Nature 402:489-495(1999).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM C).  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP SEQUENCE OF 1-26 FROM N.A.  
 RX PubMed=11829738;  
 RA Castoldi M., Chu M.-L.;  
 RT "Structural and functional characterization of the human and mouse  
 RT fibulin-1 gene promoters: role of Sp1 and Sp3.";  
 RL Biochem. J. 362:41-50(2002).  
 RN [8]  
 RP SEQUENCE OF 30-44.  
 RX MEDLINE=89354537; PubMed=2527614;  
 RA Argaves W.S., Dickerson K., Burgess W.H., Ruoslahti E.;  
 RT "Fibulin, a novel protein that interacts with the fibronectin  
 RT receptor beta subunit cytoplasmic domain.";

RL Cell 58:623-629(1989).  
 RN [9]  
 RP SELF-ASSOCIATION AND INTERACTION WITH FN1.  
 RX PubMed=1400330;  
 RA Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K.,  
 RA Argraves W.S.;  
 RT "Fibulin binds to itself and to the carboxyl-terminal heparin-binding  
 RT region of fibronectin.";  
 RL J. Biol. Chem. 267:20120-20125(1992).  
 RN [10]  
 RP POSSIBLE FUNCTION.  
 RX PubMed=7534784;  
 RA Roark E.F., Keene D.R., Haudenschild C.C., Godyna S., Little C.D.,  
 RA Argraves W.S.;  
 RT "The association of human fibulin-1 with elastic fibers: an  
 RT immunohistological, ultrastructural, and RNA study.";  
 RL J. Histochem. Cytochem. 43:401-411(1995).  
 RN [11]  
 RP INTERACTION WITH FGB.  
 RX PubMed=7642629;  
 RA Tran H., Tanaka A., Litvinovich S.V., Medved L.V., Haudenschild C.C.,  
 RA Argraves W.S.;  
 RT "The interaction of fibulin-1 with fibrinogen. A potential role in  
 RT hemostasis and thrombosis.";  
 RL J. Biol. Chem. 270:19458-19464(1995).  
 RN [12]  
 RP DEVELOPMENTAL STAGE.  
 RX PubMed=8737292;  
 RA Miosge N., Gotz W., Sasaki T., Chu M.-L., Timpl R., Herken R.;  
 RT "The extracellular matrix proteins fibulin-1 and fibulin-2 in the  
 RT early human embryo.";  
 RL Histochem. J. 28:109-116(1996).  
 RN [13]  
 RP INDUCTION.  
 RX MEDLINE=96133928; PubMed=8552629;  
 RA Clinton G.M., Rougeot C., Derancourt J., Roger P., Defrenne A.,  
 RA Godyna S., Argraves W.S., Rochefort H.;  
 RT "Estrogens increase the expression of fibulin-1, an extracellular  
 RT matrix protein secreted by human ovarian cancer cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:316-320(1996).  
 RN [14]  
 RP CALCIUM, SELF-ASSOCIATION, AND FN1-BINDING SITES.  
 RX PubMed=9278415;  
 RA Tran H., VanDusen W.J., Argraves W.S.;  
 RT "The self-association and fibronectin-binding sites of fibulin-1 map  
 RT to calcium-binding epidermal growth factor-like domains.";  
 RL J. Biol. Chem. 272:22600-22606(1997).  
 RN [15]  
 RP ROLE IN TUMOR FORMATION AND INVASION.  
 RX PubMed=9393974;  
 RA Qing J., Maher V.M., Tran H., Argraves W.S., Dunstan R.W.,  
 RA McCormick J.J.;  
 RT "Suppression of anchorage-independent growth and matrigel invasion and  
 RT delayed tumor formation by elevated expression of fibulin-1D in human  
 RT fibrosarcoma-derived cell lines.";  
 RL Oncogene 15:2159-2168(1997).  
 RN [16]

RP INDUCTION.  
RX PubMed=9811350;  
RA Roger P., Pujol P., Lucas A., Baldet P., Rochefort H.;  
RT "Increased immunostaining of fibulin-1, an estrogen-regulated protein  
RT in the stroma of human ovarian epithelial tumors.";  
RL Am. J. Pathol. 153:1579-1588(1998).  
RN [17]  
RP ROLE IN TUMOR FORMATION AND INVASION.  
RX PubMed=9466671;  
RA Hayashido Y., Lucas A., Rougeot C., Godyna S., Argraves W.S.,  
RA Rochefort H.;  
RT "Estradiol and fibulin-1 inhibit motility of human ovarian- and  
RT breast-cancer cells induced by fibronectin.";  
RL Int. J. Cancer 75:654-658(1998).  
RN [18]  
RP INTERACTION WITH NOV.  
RX PubMed=9927660;  
RA Perbal B., Martinerie C., Sainson R., Werner M., He B., Roizman B.;  
RT "The C-terminal domain of the regulatory protein NOVH is sufficient to

Query Match 27.7%; Score 701.5; DB 1; Length 703;  
Best Local Similarity 34.4%; Pred. No. 8.6e-45;  
Matches 162; Conservative 66; Mismatches 150; Indels 93; Gaps 22;

```

QY      16 CLPSPGNAQAQCTNGFDLDRSQGLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV 75
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      288 CRP-----KLQCKSGFIQD-ALGNCIDINECLISAPCPIGHTCINTEGYSYC----- 334

QY      76 YRGPYSNPYSTPYSGPYAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD 134
      : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      335 -----QKNVPN-----CGRGYHLNNEEGTRCVDVDECAFP 363

QY      135 SHQCNPQTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS 189
      : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      364 AEPCKGKHRCVNSPGSFRCECKTGYYFDGISRMCVDVNECQRYPGRLCGHKCENTLGSYL 423

QY      190 CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDM 248
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      424 CSCSVGFRLSVDGRSCEDINECSS-SPCSQECANVGSYQCYCRRGYQLSDVDGVTCEDI 482

QY      249 DECSF--SEFLQHECVNQPGTYFCSCP-PGYILLDDNRSQDINECEHRNHTCNLQQTIC 305
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      483 DECALPTGGHICSYRCINIPGSFQCSCPSSGYRLAPNRCNQDIDECVTGIHNCINETC 542

QY      306 YNLQGGFKCIDPIRCEEPYLRISDN-----RCMCPAENPGCRDQPFTILYRDMDVV 356
      : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      543 FNIQGGFRCL-AFECPENYRRSAATLQKEKTDTRCI----KSCRPNDVTCVPDPVHTI 596

QY      357 SGRSV-----PADIFQMQA-TTRYPG--AYYIFQIKSGNEGREF----YMRQTG 398
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      597 SHTVISLPTFREFTREEIIFLRAITPPHPASQANIIFDITEGNLRDSFDIIKRYM--DG 654

QY      399 PISATLVMTMPIKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 448
      : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      655 MTVGVVRQVRPIVGPFHVLKLEMNYYVGGVVSHR--NVNVNRIFFVSEYWF 703

```



## RESULT 14

## FBL1\_MOUSE

ID FBL1\_MOUSE STANDARD; PRT; 705 AA.  
AC Q08879; Q08878; Q8C3B1; Q91ZC9; Q922K8;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Fibulin-1 precursor (Basement-membrane protein 90) (BM-90).  
GN FBLN1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS C AND D), AND LIGANDS INTERACTION.  
RX MEDLINE=93358897; PubMed=8354280;  
RA Pan T.-C., Kluge M., Zhang R.Z., Mayer U., Timpl R., Chu M.-L.;  
RT "Sequence of extracellular mouse protein BM-90/fibulin and its  
RT calcium-dependent binding to other basement-membrane ligands";  
RL Eur. J. Biochem. 215:733-740(1993).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM C).  
RC STRAIN=CS7BL/6J; TISSUE=Head, and Urinary bladder;  
RX MEDLINE=22354683; PubMed=12466851;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RL Nature 420:563-573(2002).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM C).  
RC TISSUE=Breast tumor;  
RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP SEQUENCE OF 1-26 FROM N.A.  
 RX PubMed=11829738;  
 RA Castoldi M., Chu M.-L.;  
 RT "Structural and functional characterization of the human and mouse  
 RT fibulin-1 gene promoters: role of Sp1 and Sp3.";  
 RL Biochem. J. 362:41-50(2002)..  
 RN [5]  
 RP CHARACTERIZATION OF NID AFFINITY.  
 RX PubMed=7844816;  
 RA Sasaki T., Kostka G., Goehring W., Wiedemann H., Mann K., Chu M.-L.,  
 RA Timpl R.;  
 RT "Structural characterization of two variants of fibulin-1 that differ  
 RT in nidogen affinity.";  
 RL J. Mol. Biol. 245:241-250(1995).  
 RN [6]  
 RP DEVELOPMENTAL STAGE.  
 RX PubMed=8850569;  
 RA Zhang H.-Y., Timpl R., Sasaki T., Chu M.-L., Ekblom P.;  
 RT "Fibulin-1 and fibulin-2 expression during organogenesis in the  
 RT developing mouse embryo.";  
 RL Dev. Dyn. 205:348-364(1996).  
 RN [7]  
 RP NID-BINDING SITE.  
 RC STRAIN=129/Sv;  
 RX PubMed=9299350;  
 RA Adam S., Goehring W., Wiedemann H., Chu M.-L., Timpl R., Kostka G.;  
 RT "Binding of fibulin-1 to nidogen depends on its C-terminal globular  
 RT domain and a specific array of calcium-binding epidermal growth  
 RT factor-like (EG) modules.";  
 RL J. Mol. Biol. 272:226-236(1997).  
 RN [8]  
 RP BINDING TO LAMA2.  
 RX PubMed=10022829;  
 RA Talts J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;  
 RT "Binding of the G domains of laminin alpha1 and alpha2 chains and  
 RT perlecan to heparin, sulfatides, alpha-dystroglycan and several

RT extracellular matrix proteins.";  
 RL EMBO J. 18:863-870(1999).  
 RN [9]  
 RP INTERACTION WITH AGC1 AND CSPG2.  
 RX PubMed=10400671;  
 RA Aspberg A., Adam S., Kostka G., Timpl R., Heinigaard D.;  
 RT "Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and  
 RT versican.";  
 RL J. Biol. Chem. 274:20444-20449(1999).  
 RN [10]  
 RP INTERACTION WITH NID.  
 RX PubMed=11589703;  
 RA Ries A., Goehring W., Fox J.W., Timpl R., Sasaki T.;  
 RT "Recombinant domains of mouse nidogen-1 and their binding to basement  
 RT membrane proteins and monoclonal antibodies.";  
 RL Eur. J. Biochem. 268:5119-5128(2001).  
 RN [11]  
 RP DOWN-REGULATION BY GLUCOCORTICOIDS.  
 RX PubMed=11737251;  
 RA Gu Y.-C., Talts J.F., Gullberg D., Timpl R., Ekblom M.;  
 RT "Glucocorticoids down-regulate the extracellular matrix proteins  
 RT fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";  
 RL Eur. J. Haematol. 67:176-184(2001).  
 RN [12]  
 RP TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.  
 RX PubMed=11238726;  
 RA Ohsawa I., Takamura C., Kohsaka S.;  
 RT "Fibulin-1 binds the amino-terminal head of beta-amyloid precursor  
 RT protein and modulates its physiological function.";  
 RL J. Neurochem. 76:1411-1420(2001).  
 RN [13]  
 RP INTERACTION WITH E6, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.  
 RX PubMed=12200142;  
 RA Du M., Fan X., Hong E., Chen J.J.;  
 RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";  
 RL Biochem. Biophys. Res. Commun. 296:962-969(2002).  
 RN [14]  
 RP DEVELOPMENTAL STAGE.  
 RX PubMed=11836357;  
 RA Debeer P., Schoenmakers E.F.P.M., Twal W.O., Argraves W.S.,  
 RA De Smet L., Fryns J.-P., Van De Ven W.J.M.;  
 RT "The fibulin-1 gene (FBLN1) is disrupted in a t(12;22) associated with  
 RT a complex type of synpolydactyly.";  
 RL J. Med. Genet. 39:98-104(2002).  
 CC -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.  
 CC May play a role in cell adhesion and migration along protein  
 CC fibers within the extracellular matrix (ECM). Could be important  
 CC for certain developmental processes and contribute to the  
 CC supramolecular organization of ECM architecture, in particular to  
 CC those of basement membranes.  
 CC -!- SUBUNIT: Interacts with itself and with various extracellular  
 CC matrix components such as FN1, LAMA1, LMA2, NID, AGC1, CSPG2 and  
 CC type IV collagen. Interacts also with papillomavirus E6 proteins.  
 CC Binding analysis demonstrated for isoform C a 100-fold stronger  
 CC binding to the basement membrane protein NID than for isoform D.  
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.  
 CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=D;  
 CC IsoId=Q08879-1; Sequence=Displayed;  
 CC Name=A;  
 CC IsoId=Q08879-3; Sequence=Not described;  
 CC Name=B;  
 CC IsoId=Q08879-4; Sequence=Not described;  
 CC Name=C;  
 CC IsoId=Q08879-2; Sequence=VSP\_001386;  
 CC Note=Conflict E -> A at position 571 of isoform C (Ref.1);  
 CC -!- TISSUE SPECIFICITY: Detected in most organs (brain, heart, lung,  
 CC spleen, liver and kidney). Neurons are the predominant source of  
 CC production in the brain. Not expressed significantly by astrocytes  
 CC or microglia.  
 CC -!- DEVELOPMENTAL STAGE: The differential expression of the fibulin  
 CC family contributes to the formation of molecularly distinct  
 CC extracellular matrices already during early developmental stages  
 CC of a large number of tissues. Increase expression at neonate stage  
 CC in the brain. Expressed in interdigital regions of the handplate  
 CC of a 12 dpc embryo and in the lateral perichondrial region.  
 CC Similar expression persists in the 13 dpc handplate particularly  
 CC in the perichondrial regions and apical aspects of the developing  
 CC digits.  
 CC -!- INDUCTION: Glucocorticoids suppressed mRNA expression and protein  
 CC synthesis.  
 CC -!- SIMILARITY: Belongs to the fibulin family.  
 CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.  
 CC -!- SIMILARITY: Contains 9 EGF-like domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

Query Match 27.7%; Score 700.5; DB 1; Length 705;  
 Best Local Similarity 34.7%; Pred. No. 1e-44;  
 Matches 161; Conservative 68; Mismatches 156; Indels 79; Gaps 22;

```

Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQCCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNFV 75
      | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      290 CRP-----KLQCKSGFIQD-ALGNCIDINECLISAPCPVGQTCINTEGYSYC----- 336

Qy      76 YRGPYSNPYSTPYSGPYAAAPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD 134
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      337 -----QKNVPN-----CGRGYHLNNEEGTRCVDVDECSP 365

Qy      135 SHQCNPQTQICINTEGGYTCSCTDGYWL--LEGQCCLDIDEC-RY--GYCQQLCANVPGSYS 189
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      366 AEPCKGKHCHLNSPGSPRCCKAGFYFDGISRTCDVINECQRYPGRLCGHKCENTPGSFH 425

Qy      190 CTCNPGFTLNEIDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDM 248
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      426 CSCSAGFRLSDVGRSCEDVNEC-LNSPGSQECANVYGSYQCYCRRGYQLSDVDGVTCEBDI 484

Qy      249 DECSF--SEFLQCHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTC 305
      | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db      485 DECALPTGGHICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCISINETC 544

Qy      306 YNLQGGFKCIDPIRCEEPYLISDN-----RCM--CPAENPGC-RDQPPTILYRDM 353
  
```

```

Db      545 FNIQGSFRCLSL-FCPENYRRSADTFRQEKTDTRVCIKSCRPNDEACVRDPVHTVSHTVI 603
Qy      354 DVVSGRSV--PADIFQMQATT-RYPG--AYYIFQIKSGNEGREFYM---RQTGPISATLV 405
Db      604 SLPTFRFEFRPEEIIFLRAVTPLYPANQADIIFDITEGNLRDSFDIIKRYEDGMTVGVVVR 663
Qy      406 MTRPIKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 448
Db      664 QVRPIVGPFYAVLKLEMMNYVLGGVVSHR--NVNVNHVIFVSEYWF 705

```

RESULT 15

FBL1\_BRARE

```

ID      FBL1_BRARE      STANDARD;      PRT;      681 AA.
AC      042182; 042183;
DT      15-SEP-2003 (Rel. 42, Created)
DT      15-SEP-2003 (Rel. 42, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Fibulin-1 precursor.
GN      FBLN1.
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS C AND D).
RA      Zhang H.-Y., Lardelli M., Ekblom P.;
RT      "Sequence of zebrafish fibulin-1 and its expression in developing
RT      heart and other embryonic organs.";
RL      Dev. Genes Evol. 207:340-351(1997).
CC      -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.
CC      May play a role in cell adhesion and migration along protein
CC      fibers within the extracellular matrix (ECM). Could be important
CC      for certain developmental processes and contribute to the
CC      supramolecular organization of ECM architecture, in particular to
CC      those of basement membranes.
CC      -!- SUBUNIT: Interacts with itself and with various extracellular
CC      matrix components such as FN1, LAMA1, NID, AGC1 and CSPG2.
CC      -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=D;
CC      IsoId=042182-1; Sequence=Displayed;
CC      Name=C;
CC      IsoId=042182-2; Sequence=VSP_007379;
CC      -!- DEVELOPMENTAL STAGE: Isoform C is detected in the later blastula
CC      period, 4 h after fertilization. Isoform D is not detected at this
CC      stage, it first appears during the gastrula period in 8-h-old
CC      embryos. Expression of both isoforms is then maintained throughout
CC      development. During later developmental stages, prominent
CC      expression is seen in regions where tissue compartments are
CC      continuously moving in relation to each other.
CC      -!- SIMILARITY: Belongs to the fibulin family.
CC      -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC      -!- SIMILARITY: Contains 9 EGF-like domains.

```

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF013751; AAB80944.1; -.
DR EMBL; AF013752; AAB80945.1; -.
DR HSSP; P35555; 1EMN.
DR ZFIN; ZDB-GENE-990415-73; fb1n1.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001673; S_mold_repeat.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF00008; EGF; 4.
DR SMART; SM00104; ANATO; 2.
DR SMART; SM00179; EGF_CA; 5.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 6.
KW Signal; Alternative splicing; Glycoprotein; Extracellular matrix;
KW Repeat; EGF-like domain; Calcium-binding.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 681 FIBULIN-1.
FT DOMAIN 29 63 ANAPHYLATOXIN-LIKE 1.
FT DOMAIN 68 107 ANAPHYLATOXIN-LIKE 2.
FT DOMAIN 108 139 ANAPHYLATOXIN-LIKE 3.
FT DOMAIN 158 192 EGF-LIKE 1.
FT DOMAIN 193 238 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 239 284 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 285 331 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 332 373 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 374 415 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 416 455 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 456 499 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 500 554 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT DISULFID 29 55 BY SIMILARITY.
FT DISULFID 30 62 BY SIMILARITY.
FT DISULFID 43 63 BY SIMILARITY.
FT DISULFID 72 103 BY SIMILARITY.
FT DISULFID 85 104 BY SIMILARITY.
FT DISULFID 106 125 BY SIMILARITY.
FT DISULFID 107 138 BY SIMILARITY.
FT DISULFID 114 139 BY SIMILARITY.
FT DISULFID 162 171 BY SIMILARITY.
FT DISULFID 167 176 BY SIMILARITY.
FT DISULFID 178 191 BY SIMILARITY.
FT DISULFID 197 210 BY SIMILARITY.
FT DISULFID 204 219 BY SIMILARITY.
FT DISULFID 225 237 BY SIMILARITY.

```

FT	DISULFID	243	256	BY SIMILARITY.
FT	DISULFID	250	265	BY SIMILARITY.
FT	DISULFID	271	283	BY SIMILARITY.
FT	DISULFID	289	301	BY SIMILARITY.
FT	DISULFID	317	330	BY SIMILARITY.
FT	DISULFID	336	348	BY SIMILARITY.
FT	DISULFID	343	357	BY SIMILARITY.
FT	DISULFID	359	372	BY SIMILARITY.
FT	DISULFID	378	390	BY SIMILARITY.
FT	DISULFID	386	399	BY SIMILARITY.
FT	DISULFID	401	414	BY SIMILARITY.
FT	DISULFID	420	429	BY SIMILARITY.
FT	DISULFID	440	454	BY SIMILARITY.
FT	DISULFID	460	473	BY SIMILARITY.
FT	DISULFID	469	482	BY SIMILARITY.
FT	DISULFID	484	498	BY SIMILARITY.
FT	DISULFID	504	517	BY SIMILARITY.
FT	DISULFID	511	526	BY SIMILARITY.
FT	DISULFID	531	553	BY SIMILARITY.
FT	CARBOHYD	173	173	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	542	681	RPRVDRADIIRCCKSCQHNDISCVLNPILSHSHTAISLPTF

FT				REFNKPPEEIVFLRSPPTPHLPHMDSPEIVDILEGNIQNSF
FT				DIKRLDHGMIUGVVKQVRPLVGPVRTVLKLANNYVTNGVV
FT				SHRNIINVRIYVSEFWF -> RCERLSCNESNECMAPTRRI
FT				TTYQLTFPAKIPVPTDLFRMGPSNTALGDDIEVAIVDGNRD
FT				GFFAAKRLDHGGVVLVLQKPIAWPQDFQIALEMKLRFGHLS
FT				IYLFKIRPVRHARRHQORY (in isoform C).
FT				/FTId=VSP_007379.

SQ SEQUENCE 681 AA; 74459 MW; 175C966305A46699 CRC64;

Query Match 24.9%; Score 631; DB 1; Length 681;  
 Best Local Similarity 32.6%; Pred. No. 1.4e-39;  
 Matches 153; Conservative 65; Mismatches 162; Indels 90; Gaps 22;

Qy	16	CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMCMVNQNGGYLCIPRTNPV	75
Db	265	CRP-----RMQCAAGFIQD-ALGSCIDINECVSVTALSRG-QMCFNTVGSFICQQRHS---	314
Qy	76	YRGPYSNPYSTPYSGPYFAAAPPLSAPNYPTISRPLICRFQYQMD-ESNQCDVDECATD	134
Db	315	-----VTQGRGYHLNAEGTRCVDIDECAGP	339
Qy	135	SHQCNPQTICINTEGGYTCSCTDGYWL--LEGQCLDIDECRYGY---CQQLCANVPGSY	188
Db	340	DNSCD-GHGCINLVGSYRCBCTGFIENFNSISRCEDIDECR-NYPGRLLCAHKCENILGSY	397
Qy	189	SCTCNPGFTLNEIDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEB-DGVHCSD	247
Db	398	KCSCTAGFKLADDRNDDVNECES-SPCSQGCANVYGSYQSYCRRGYQLSDADGITCED	456
Qy	248	MDECSF--SEFLCQHECVNPGTYFCSCP-PGYILLDDNRSCQDINECHERNHTCNLQQT	304
Db	457	IDECALPTGGHICSYRCHNTPGSHCTCPASGYTLAANGRSCQDIDECLTGTHSCSESES	516
Qy	305	CYNLQGGFKCIDPIRCEPYLRISDN-----RCM--CPAENPGCRDQPFTILYRD	352
Db	517	CFNIQGGFRCLS-FDCPANYYRSGDTRPRVDRADIIRCCKSCQHNDISCVLNP--ILSHS	573

Qy	353	MDVVS-----GRSVPADIFQMQATT-----RYPGAYYIFQIKSGNEGREFYMRQT---GP 399
	:	:   : :   : :   : :   : :
Db	574	HTAISLPTTFREFNKPEEIVFLRSPTPTHLPHMDSPEIVYDILEGNIQNSFDIIRKLDHGM 633
Qy	400	ISATLVMTRPIKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 448
	:	:   :   :   :   : :   : :   : :   : :
Db	634	IVGVVKQVRPLVGPVRTVLKAMNYVTNGVVSHR--NIINVRIYVSEFWF 681

Search completed: January 9, 2004, 12:34:05  
 Job time : 11.287 secs



OM protein - protein search, using sw model

Run on: January 9, 2004, 12:32:07 ; Search time 34.4615 Seconds  
(without alignments)  
3354.684 Million cell updates/sec

Title: US-09-674-379A-13  
Perfect score: 2533  
Sequence: 1 MPGIKRILTVTILALCLPSP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriaphage:\*  
17: sp\_archaeophages:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description
-----						

1	1289	50.9	443	4	Q96TF5	Q96tf5 homo sapien
2	1283	50.7	443	11	Q9JM06	Q9jm06 mus musculus
3	1266	50.0	443	4	Q9H3D5	Q9h3d5 homo sapien
4	1100	43.4	493	11	Q8BPB5	Q8bpb5 mus musculus
5	960.5	37.9	387	11	Q8K0J4	Q8k0j4 mus musculus
6	743	29.3	685	11	Q922K8	Q922k8 mus musculus
7	743	29.3	685	11	Q8C3B1	Q8c3b1 mus musculus
8	737	29.1	683	4	Q8TBH8	Q8tbh8 homo sapien
9	735.5	29.0	1174	11	Q99K58	Q99k58 mus musculus
10	728	28.7	598	6	Q8MJJ9	Q8mjj9 cercopithec
11	722	28.5	704	13	O73774	O73774 gallus gall
12	711.5	28.1	576	4	Q9Y3V7	Q9y3v7 homo sapien
13	710.5	28.0	1231	4	Q8IUI1	Q8iui1 homo sapien
14	709.5	28.0	1231	4	Q8IUI0	Q8iui0 homo sapien
15	696.5	27.5	638	4	Q8NBH6	Q8nbh6 homo sapien
16	676	26.7	495	4	Q9HBQ5	Q9hbq5 homo sapien
17	631	24.9	681	13	O42182	O42182 brachydanio
18	587	23.2	698	5	Q9V4B8	Q9v4b8 drosophila
19	583	23.0	554	4	Q9UH16	Q9uh16 homo sapien
20	558.5	22.0	1409	5	Q9VS89	Q9vs89 drosophila
21	548	21.6	2673	4	Q96SC3	Q96sc3 homo sapien
22	537	21.2	5636	4	Q96RW7	Q96rw7 homo sapien
23	528.5	20.9	787	11	Q8K061	Q8k061 mus musculus
24	527.5	20.8	2872	11	Q9WUH8	Q9wuh8 rattus norv
25	524.5	20.7	741	4	Q96K89	Q96k89 homo sapien
26	522.5	20.6	1398	13	Q8AXM6	Q8axm6 xenopus lae
27	521.5	20.6	3857	11	O88840	O88840 mus musculus
28	521	20.6	1389	11	Q8CG18	Q8cg18 mus musculus
29	521	20.6	1713	11	Q8CG19	Q8cg19 mus musculus
30	520.5	20.5	1399	13	Q8JFZ4	Q8jtz4 xenopus lae
31	519.5	20.5	2809	4	Q96JP8	Q96jp8 homo sapien
32	517	20.4	1713	11	O88349	O88349 mus musculus
33	516.5	20.4	708	13	P87363	P87363 gallus gall
34	515.5	20.4	2906	11	Q9WUH9	Q9wuh9 rattus norv
35	511.5	20.2	729	11	Q8BNH3	Q8bnh3 mus musculus
36	511.5	20.2	937	5	Q9BLJ1	Q9blj1 ciona intes
37	508	20.1	188	11	Q8R1U8	Q8rlu8 mus musculus
38	495.5	19.6	1963	6	Q28019	Q28019 bos taurus
39	495	19.5	746	4	Q96HB9	Q96hb9 homo sapien
40	495	19.5	893	6	Q8MJK0	Q8mjk0 cercopithec
41	495	19.5	1256	4	Q9NS15	Q9ns15 homo sapien
42	495	19.5	1382	4	Q9H7K2	Q9h7k2 homo sapien
43	494.5	19.5	1095	11	Q60784	Q60784 mus musculus
44	492.5	19.4	1764	11	O35806	O35806 rattus norv
45	491	19.4	517	4	Q9NFP01	Q9np01 homo sapien

# ALIGNMENTS

## RESULT 1

### Q96TF5

ID Q96TF5 PRELIMINARY; PRT; 443 AA.  
AC Q96TF5;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Mutant p53 binding protein 1 (MBP1).  
GN MBP1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tanka S.;  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Tanaka S., Sugimachi K., Sugimachi K.;  
RT "Human mutant p53 binding protein (MBP1).";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB030655; BAA92880.1; -.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR001491; Thrombomodulin.  
DR Pfam; PF00008; EGF; 4.  
DR PRINTS; PR00907; THROMBOMODULN.  
DR SMART; SM00179; EGF\_CA; 4.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 4.  
DR PROSITE; PS01186; EGF\_2; 4.  
DR PROSITE; PS01187; EGF\_CA; 6.  
KW EGF-like domain.  
SQ SEQUENCE 443 AA; 49421 MW; 9CE175F4F388A56D CRC64;

Query Match 50.9%; Score 1289; DB 4; Length 443;  
Best Local Similarity 49.9%; Pred. No. 7.4e-118;  
Matches 226; Conservative 74; Mismatches 131; Indels 22; Gaps 5;

QY 1 MPGIKRLITVTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG 55  
:| | : : : | | | : : : | | | : | | | | | | | |  
Db 8 LPGSLLLWALLLLLLLGSASPQDSEEPDSYTECTDGYEWDPSQHC RDVNECLTIPEACKG 67  
QY 56 DMMCVNQNGGYLCIPRTNPVVRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRF 115  
: | | : | | | | : | : | : | | : | | | | | | | |  
Db 68 EMKCINHYGGYLCIPRSAAVINDLHG-----EGP-PPVPVPAQHFN-----PCPP 111  
QY 116 GYQMDESNQCDVDDECATDSHQCNPTQICINTEGGYTCSCDTGYWLLLEGQCLDIDECRYG 175  
| | : : : | | | | | | | | | | | | | | | | : : : | | | | |  
Db 112 GYEPDDQDSCVDVDECAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYR 171  
QY 176 YCQQLCANVPGSYSTCNPNGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPG 235  
| | | | | : | | | | | | | | : | | | | | | | | | | | | | |  
Db 172 YCQHRVCNVLPGSFRQCPEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQG 231  
QY 236 YELEEDGVHCSMDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHR 295  
| | | | | | | | | | | | | | : | | | | | | | | | | | | | |  
Db 232 YELHRDGFSCSDIDECYSYSSYLQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECESG 290  
QY 296 NHTCNLQQTCTYNLQGGFKCIDPIRCEEPLYRISDNRMCPAENPGCRDQPFITILYRDMDV 355  
| | : | | | | : | | | | | | | | | | | | | | | | : : : | |  
Db 291 AHQCSEAQTCVNFHGGYRCVDTNRCVEPYIQVSENRLCPASNPLCREQPSSIVHRYMTI 350

Qy 356 VSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 415  
 Db 351 TSERSVPADVFOIQATSVYPGAYNAFQIRAGNSQGDYFIQINNVSAMVLARPVGTGPRE 410  
 Qy 416 IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448  
 Db 411 YVLDLEMTMNSLSYRASSVRLRLTVFVGAYTF 443

# RESULT 2

Q9JMO6

ID Q9JMO6 PRELIMINARY; PRT; 443 AA.  
 AC Q9JMO6;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE EGF-containing fibulin-like extracellular matrix protein 2.  
 GN EFEMP2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20435063; PubMed=10982184;  
 RA Katsanis N., Venable S., Smith J.R., Lupski J.R.;  
 RT "Isolation of a paralog of the Doyme honeycomb retinal dystrophy gene  
 RT from the multiple retinopathy critical region on 11q13.";  
 RL Hum. Genet. 106:66-72(2000).  
 DR EMBL; AF109122; AAF65189.1; -.  
 DR HSSP; P00736; IAPQ.  
 DR MGD; MGI:1891209; Efemp2.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR001491; Thrbomoduln.  
 DR Pfam; PF00008; EGF; 4.  
 DR PRINTS; PR00907; THRBOMODULN.  
 DR SMART; SM00179; EGF\_CA; 4.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 4.  
 DR PROSITE; PS01186; EGF\_2; 4.  
 DR PROSITE; PS01187; EGF\_CA; 6.  
 KW EGF-like domain; Matrix protein.  
 SQ SEQUENCE 443 AA; 49452 MW; 5AEC2A91048B336A CRC64;

Query Match 50.7%; Score 1283; DB 11; Length 443;  
 Best Local Similarity 49.9%; Pred. No. 2.9e-117;  
 Matches 226; Conservative 70; Mismatches 135; Indels 22; Gaps 4;

Qy 1 MPGIKRILTVTILALCLFSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG 55  
 Db 8 LPGSLLLWAFLLLLGAASPDQPEEPDSYTECTDGYEWDADSQHCRDVECLTIPEACKG 67  
 Qy 56 DMMCVNQNGGYLCIPRTNPVYRGFPYSNPYSTPYSGPYPAAPPLSAPNYPTISRLPICRF 115  
 Db 68 EMKCINHYGGYLCIPRSAAVINDLHG-----EGPPPPAA-----HAQQPNPCPQ 111

Qy	116	GYQMDSESNQCVDVDECATDSHQCNPTQICINTBGGYTCSCTDGYWLLLEGQCLDIDECRYG	175
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	112	GEPPDEQESCDVDVECTQALHDCRSPQDCHNLPGSYQCTCPDGYRKIGPEPCVDIDECRYR	171
Qy	176	YCQQLCANVPGSGYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPG	235
		:   :   :           :   :                     :   :   :   :   :	
Db	172	YCQHRCVNLPGSPRCQCCEPGQLGPNNRSCVDVNECDMGAPCBQRCFNSYGTFLCRCNQG	231
Qy	236	YELEEDGVHCSMDMECSFSEFLCQHECVNPGTYFSCPPGYILLDDNRSCQDINECEHR	295
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	232	YELHRDGFSCSDIDECGYSSYLQYRCVNBPGRFSCBPCQGYQLL-ATRLQDQIDECETG	290
Qy	296	NHTCNLQQTCTYNLQGGFKCIDPICEBPYLIRISDNRCMCPAENPGCRDPPTILYRMDV	355
		:         : :   :       : :   :   :   :   :   :   :   :   :   :   :	
Db	291	AHQCEAQTCTVNFHGGYRCVDTNRCVEPYQVSDNRCLCPASNPLCREQPSIVHRYMSI	350
Qy	356	VSGRSPVADIFQMQATTRYPGAYYIFQIKSGNEGREGFYMRQTPGISATLVMTRPIKGP	415
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	351	TSERSVPADVFOIQATSVYPGAYNAFQIRSGNTQGDFFYIRINNVSAMVLARPVTPGR	410
Qy	416	IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPP	448
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	411	YVLDEMTVMTNSLMSYRASSVLRLTVFVGAYTF	443

## 09H3D5

```
ID Q9H3D5      PRELIMINARY;      PRT;    443 AA.
AC Q9H3D5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fibulin-like extracellular matrix protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Seibold S., Marx M.;
RT "Cloning of a new fibulin-like gene.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF124486; AAG45245.1; -.
DR HSSP; P35555; 1EMN.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001491; ThrmBomoduln.
DR Pfam; PF00008; EGF; 3.
DR PRINTS; PR00907; THRMBOMODULN.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS01187; EGF_CA; 5.
KW EGF-like domain; Matrix protein.
SQ SEQUENCE 443 AA; 49535 MW; D91784BF36A8A060 CRC64;
```

Query Match 50.0%; Score 1266; DB 4; Length 443;  
 Best Local Similarity 49.2%; Pred. No. 1.3e-115;  
 Matches 223; Conservative 74; Mismatches 134; Indels 22; Gaps 5;

```

Qy      1  MPGKIRILVTITLALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG 55
      :|| : : :| | | : : : :|| : : | | | :|| ||||| :|
Db      8  LPGSLLLWALLLLLLGSGASPDQSEEPDSYTECTDGYEWDPSQHC RDVNECLTIPEACKG 67

Qy      56 DMMCVNQNGGYLCIPRTNPVYRGYPSPYSTPYSGPYAPPAAPLSAPNYPTISRPLICRF 115
      :| | :| ||||| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      68 EMKCTINHYGGYLCIPRSAAVINDLHG-----EGP-PPVPVPAQHFN-----PCPP 111

Qy      116 GYQMDESNCQVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYG 175
      || : : : ||||| | :| :| :| :| :| :| :| :| :| :| :| :|
Db      112 GYEPDDQDSCVDVDECAQALHDDRPSQDCHNLSSGSYQCTCPDGYRKIGPECVDIDECRYR 171

Qy      176 YCQQLCANVFGSYSTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNITYGSFICRCDPG 235
      || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      172 YCQHRVCNLPFGSRFCQCEPGFQLGPNNRSCVDVNECDMGAPCBQRCFNSYGTFLCRCHQG 231

Qy      236 YELEEDGVHCSMDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHR 295
      ||| | | ||| :||| :| :| :| :| :| :| :| :| :| :| :| :|
Db      232 YELHRDGFSCSDIDECSSYSSYLQYRCVNEPGRFSCHPQGYQLL-ATRLCQDIDECESG 290

Qy      296 NHTCNLQQTCTYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENFGCRDOPFTILYRDMDV 355
      | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      291 AHQCSEAQTCTVNFHGGYRCVDTNRCVEPYIQVSENRCLCPASNFLCREQPSIVHYRMTI 350

Qy      356 VSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRE 415
      | | ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      351 TSERM RPADVFQIQATSVYPGAYNAFQIRAGNSQGDYFIRQINNVSAMLVLARPVTPGRE 410

Qy      416 IQLDLEMITVNTVINFRGSSVIRLIYVSQYPF 448
      ||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      411 YVLDLEMTVMNSLMSYRASSVLRLTVFVGAYTF 443
  
```

#### RESULT 4

##### Q8BPB5

```

ID      Q8BPB5      PRELIMINARY;      PRT;      493 AA.
AC      Q8BPB5;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Epidermal growth factor-containing fibulin-like extracellular matrix
DE      protein 1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Xiphoid cartilage;
RX      MEDLINE=22354683; PubMed=12466851;
RA      The FANTOM Consortium,
RA      the RIKEN Genome Exploration Research Group Phase I & II Team;
RT      "Analysis of the mouse transcriptome based on functional annotation of
  
```

RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK077302; BAC36738.1; -.  
 SQ SEQUENCE 493 AA; 54952 MW; 9CEDC7BF2FF9430F CRC64;

Query Match 43.4%; Score 1100; DB 11; Length 493;  
 Best Local Similarity 42.0%; Pred. No. 2.8e-99;  
 Matches 206; Conservative 72; Mismatches 161; Indels 52; Gaps 6;

```

Qy      8 LTVTILALCLPSPGNAQ-----AQTNGFDLDRQSGQLDIDECRTIPEACRGDMMCVNQ 62
      | :|:| | | | : |||:|:| | || |||| :|:|:| | |||
Db      5 LFLTMLTLALVKSQYTEETITYTQCTDGYEWDPIRQCKDIDECDIVPDACKGGMKCVNH 64

Qy     63 NGGYLCIPRTNPVYRGPSYNPYSTPYS-----GPYPAAAPP 98
      |||||:|:| : || : || : | :|:|
Db     65 YGGYLCCLPKTAQIIIVNNEHPQOETPAEEASSGATTGTVAARSMATSGVVPVGGGFMASATA 124

Qy     99 LSAPNYPT-----ISRPLICRFYQMDENSNQCVDVDECATDSHQC 138
      :: | | : | ||: | | | :||| : :| |
Db    125 VAGFEVQTGRNNFVIRRNPA DPQRIPSNPSHRIQCAAGYEQSEHNVCQDIDECTSGTHNC 184

Qy    139 NPTQICINTEGGYTCSTDGYNLLEGGQLDIDECRY-GYCCQLCANVPGSYSTCNPGFT 197
      |:||| | :| | || |||:|||| | | | | |||:| | :|:|
Db    185 RTDQVCINLRGSFTQCCLPGYQKRGEQCVDIDECTVPFYCHQRCVNTPGSFYCQCSPGFQ 244

Qy    198 LNEGGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFL 257
      | : :|:|:| | | | | ||||:|: ||| | :|:|:| | :|
Db    245 LAANNYTCVDINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEBDIDECRTSSYL 304

Qy    258 CQHECVNQPGTYFCSCP PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDP 317
      ||:|:|:|:| :| | | | :|:|:|:| | | :|:|:|:|:|
Db    305 CQYQCVNEPGKFSMCPQGYEVV-RSRTCQDINECETNE-CREDEMCMNYHGGFRCYPR 362

Qy    318 IRCPEPYLRISDNRCMPAENPGCRDQPPTILYRDMDVSGRSVPADIFQMQATTRYPGA 377
      |:| :|:|:|:| | ||:| :|:|:| :| | ||||:|:|:| |
Db    363 NPCQDHYVLTSENRCVCPVSNTMCRELPQSIVYKYSIRSDRSVPSDIFIQIATMIYANT 422

Qy    378 YYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVI 437
      |:|:|:|:| |||:| | |:| | |:| :| ||| :|:|:|:|:|:| | | |
Db    423 INTFRIKSGNENGEPYLRQTSVPVSAMLVLVKSLSGPREYIVDLEMLTVSSIGTFRITSSVL 482

Qy     438 RLRIYVSQYPF 448
      || | | : |
Db     483 RLTIIVGPFSF 493
  
```

# RESULT 5

Q8K0J4

ID Q8K0J4 PRELIMINARY; PRT; 387 AA.  
 AC Q8K0J4;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RA Strausberg R;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC031184; AAH31184.1; -.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR006210; IEGF.  
 DR Pfam; PF00008; EGF; 3.  
 DR SMART; SM00181; EGF; 5.  
 DR SMART; SM00179; EGF\_CA; 5.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 4.  
 DR PROSITE; PS01186; EGF\_2; 4.  
 DR PROSITE; PS01187; EGF\_CA; 5.  
 KW Hypothetical protein.  
 SQ SEQUENCE 387 AA; 43334 MW; EE88DC9D1422C1C7 CRC64;

Query Match 37.9%; Score 960.5; DB 11; Length 387;  
 Best Local Similarity 48.3%; Pred. No. 1e-85;  
 Matches 171; Conservative 56; Mismatches 122; Indels 5; Gaps 4;

```

Qy      96  APPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPTQICINTEGGYTCS 155
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      38  ADPQRIPISNP--SHRIQCAAGYEQSEHNVCQDIDECTSGTHNCRTDQVCINLRGSFTQC 95

Qy      156 TDGYWLLLEGQCLDIDECRY-GYCCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE 214
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      96  LPGYQKRGEQCVDIDECTVPPYCHQRCVNTPGSPFYCCSPGFLAANNYTCVDINECDAS 155

Qy      215 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPPTYFCSCP 274
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      156 NQCAQQCYNILGSFICQCNQGYELSSDRLNCEIDIDECTSSYLCQYQCVNEPGKPFSCMCP 215

Qy      275 PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMC 334
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      216 QGYEVV-RRSTCQDINECETTNE-CREDEMCWNYHGGFRCPYPRNPQDHYVLTSENRCVC 273

Qy      335 PAENPGCRDQPFTILYRMDVVSGRSVPADIFQMATTTRYPGAYIYFIQKSGNEGREFYM 394
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      274 PVSNTMCRELPQSIYVYKMSIRSDRSVPSDIFQIQATMIYANTINTFRIKSGNENGFEYFL 333

Qy      395 RQTGPISATLVMTPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      334 RQTSPVSAMLVLVKSLSGPREYIVDLEMLTVSSIGTFRTSSVLRLLTIIVGPPSF 387
  
```

RESULT 6  
 Q922K8

ID Q922K8 PRELIMINARY; PRT; 685 AA.  
 AC Q922K8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Similar to fibulin 1.







Qy 190 CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDM 248  
 Db 426 CSCSAGFRLSVUGRSCEDVNEC-LNSPCSQBECANVYGSYQCYCRRGYQLSDVDGVTCEDI 484

Qy 249 DECSF--SEFLCQHECVNQGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQOTC 305  
 Db 485 DECALPTGGHICSYRCINIPGSFQSCSPSSGYRLAPNGRNCQDIDECVTGIHNCINETC 544

Qy 306 YNLQGGFKCIDPIRCEEPLYLRISDNRC-MCPA-ENPGCRDQPFITLYLRMDVVSGRSVPA 363  
 Db 545 FNIQGSFRCLS-FECFENYRRSADTRCERLPCHENQECPRPLRITYYHLSFPTNIQVPA 603

Qy 364 DIFQMQATTTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPKGPRIQLDLEM- 422  
 Db 604 VVFRMGPSAIVPGDSMQLAITAGNEEGFFTRKVSHHSGVVALTKEPIPEPRDLLLTVMKD 663

Qy 423 -ITVNTVINFRGSSVIRLIYVS 444  
 Db 664 LYRHGTVSSF---VAKLFIFVS 682

# RESULT 8

## Q8TBH8

ID Q8TBH8 PRELIMINARY; PRT; 683 AA.  
 AC Q8TBH8;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Fibulin 1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC022497; AAH22497.1; -.  
 DR InterPro; IPR000020; Anaphylatoxin.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR Pfam; PF01821; ANATO; 3.  
 DR Pfam; PF00008; EGF; 6.  
 DR SMART; SM00104; ANATO; 3.  
 DR SMART; SM00179; EGF\_CA; 8.  
 DR PROSITE; PS01177; ANAPHYLATOXIN\_1; 3.  
 DR PROSITE; PS01178; ANAPHYLATOXIN\_2; 3.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 4.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_CA; 8.  
 KW EGF-like domain.  
 SQ SEQUENCE 683 AA; 74423 MW; 2665A3961B6403B4 CRC64;

Query Match 29.1%; Score 737; DB 4; Length 683;  
 Best Local Similarity 35.4%; Pred. No. 1.6e-63;

Matches 157; Conservative 67; Mismatches 154; Indels 66; Gaps 17;

```

Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV 75
      | | : | | : | | | | | | | | | | | | | | | | | |
Db      288 CRP-----KLQCKSGFIQD-ALGNCIDINECLISAPCPIGHTCINTEGSYTC----- 334

Qy      76 YRGPSYNPYSTPYSGPYAAAPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD 134
      : | | : | | : | | | | | | | | | | | | | | | | |
Db      335 -----QKNVFN-----CGRGYHLNEEGTRCVDVDECAFP 363

Qy      135 SHQCNPTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS 189
      : | | : | | : | | | | | | | | | | | | | | | | |
Db      364 AEP CGKGHRCVNSPGSFRCECKTGYVFDGISRMCDVNVNECQRYPGRLCGHKCENLTGSYL 423

Qy      190 CTCNPGFTLNEEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEE-DGVHCSDM 248
      | | : | | : | | | | | | | | | | | | | | | | |
Db      424 CSCSVGFRLSVVDRGSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDI 482

Qy      249 DECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQT 305
      | | : | | : | | | | | | | | | | | | | | | | |
Db      483 DECALPTGGHICSYRCINIPGSFQCSCPSSGYRLAPNGSNCQDIDECVTGIHNC SINETC 542

Qy      306 YNLQGGFKCIDPIRCEEPYLRISDNRC-MCPA-ENPGCRDPPTILYRDMVVSGRSVPA 363
      | | : | | : | | | | | | | | | | | | | | | | |
Db      543 FNIQGGFRCL-AFECPENYRRSAATRCERLPCHENRECSKLPRLRITYYHLSFPTNIQAPA 601

Qy      364 DIFQMQATTPYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPKPGPREIQDLLEMI 423
      | | : | | : | | | | | | | | | | | | | | | | |
Db      602 VVFRMGFSAAVPGDSMQLAITGNEEGFFPTRKRVSPHSGVVVALTKPVPEPRDL-----LL 656

Qy      424 TVNTVINFRG---SSVIRLRIYVS 444
      | | : | | : | | | | | | | | | | | | | | | | |
Db      657 TVKMDLSRHGTVSSFVAKLFIFVS 680

```

# RESULT 9

Q99K58

ID Q99K58 PRELIMINARY; PRT; 1174 AA.

AC Q99K58;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Similar to fibulin 2.

GN FBLN2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC005443; AAH05443.1; -.

DR HSSP; P00736; 1APQ.

DR MGD; MGI:95488; Fbln2.

DR InterPro; IPR000020; Anaphylatoxin.

DR InterPro; IPR000152; Asx\_hydroxyl.

```
DR      InterPro; IPR001881; EGF_CA.
DR      InterPro; IPR006209; EGF_like.
DR      Pfam; PF01821; ANATO; 2.
DR      Pfam; PF00008; EGF; 6.
DR      SMART; SM00104; ANATO; 3.
DR      SMART; SM00179; EGF_CA; 9.
DR      PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
DR      PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
DR      PROSITE; PS00010; ASX_HYDROXYL; 5.
DR      PROSITE; PS01186; EGF_2; 5.
DR      PROSITE; PS01187; EGF_CA; 9.
KW      EGF-like domain.
SQ
SEQUENCE 1174 AA; 126460 MW; 8D628AC710FBA6B8 CRC64;
```

Qy		23	AQAQCTNGFLDRLQSQQCLDIDECRTIPEACRGDMMCVNQGGLYCIPRTNPVYRGPYSN	82
			:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db		782	ARQR CMDGF-LQDPEGNCVDINETCSLLBPGSCGFSICNTVGSYTC-----	826
Qy		83	FYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNQNT	141
			:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db		827	-----QRNPLVCGRGYHANEBSSECVDVNEECTGVHRCGE	862
Qy		142	QICINTEGGYTCSCTDGYW--LLEGQCLDIDECRYG--YCQQLCANVPGSYSTCNPGF	196
			:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db		863	QLCYNLPGSYRCCKEFGQRDAFGRTCIDVNECWSVSPGRLCQHTCENTPGSYRCSCAA	922
Qy		197	TLNEDGRSCQDVNECATENPCVQTVMNTYGSFICRCDPGELEEDGVHCSMDSECS-FSE	255
			:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db		923	LIAADGKHCEADVNECTR-R-CSQBECANIYGSIQCYCRQGYQLAEDGHTCTDIDECAQ	981
Qy		256	FLCQHECVNQPGTYFCSCP-PGYILLDDNRSCODINECEHRNHTCNLQOTCYNLQGGFKC	314
			:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db		982	IILCTFRCVNVPGSYQACPEQGYTMMANGRSCKDLDECALGTHNCSEAETCHNIQGSFRC	1041
Qy		315	IDPIRCEEPYLRISSNRCMPAENPGCRD-----QPFTILYRMDVVSGSRVPADIFQM	368
			:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db		1042	L-RFDCPPNYVRVSETK----ERTTCQDITECQTSPARITHYQLNFQTLGLLVPAHI	1096
Qy		369	QATTRYPGAYYIFQIKSGNEGREGFYMRQTGPISATLVMTRPRIKGPREIQLDLEM	422
			:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db		1097	GPAFAFAGDTISLTITKNEEGYPVTTRLNAYTGVSVLORSVLEPRDFALDVEM	1150

```
Q8MJJ9
ID Q8MJJ9 PRELIMINARY; PRT; 598 AA.
AC Q8MJJ9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fibulin-1c (Fragment).
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Brooke J.S., Cha J.-H., Eidels L.;  
 RT "Cloning of monkey fibulin-1c gene.";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF395659; AAM90567.1; -.  
 DR InterPro; IPR000020; Anaphylatoxin.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR006210; IEGF.  
 DR Pfam; PF01821; ANATO; 1.  
 DR Pfam; PF00008; EGF; 3.  
 DR SMART; SM00104; ANATO; 1.  
 DR SMART; SM00181; EGF; 9.  
 DR SMART; SM00179; EGF\_CA; 9.  
 DR PROSITE; PS01177; ANAPHYLATOXIN\_1; 1.  
 DR PROSITE; PS01178; ANAPHYLATOXIN\_2; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 4.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_CA; 7.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 598 AA; 65516 MW; 849BF018DF452B02 CRC64;

Query Match 28.7%; Score 728; DB 6; Length 598;  
 Best Local Similarity 34.8%; Pred. No. 1e-62;  
 Matches 158; Conservative 76; Mismatches 188; Indels 32; Gaps 16;

Qy 16 CLPSPGNAQAQ---CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPR 71  
 |: : |: | | |:: | : | | |:: | : | | |:: | : | | :  
 Db 149 CINTVGSFRCQDSSCGTGyel-TEDNSCKDIDQCESGIHNCLEPDIQCNTLGSFRCRPK 207  
 Qy 72 ---TNPVYRGYPYSNPYS----TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDEN 123  
 | : : | : | : | : | : | : | : | : | : | : | : | : | :  
 Db 208 LQCKNGFIQDALANCIDINECLSIVSAPCPTGHTCINTEGYSYTKQNVPCNCGRGYHLNEEG 267  
 Qy 124 QCVDVDECATDSSHQCNPQTICINTEGGYTCSCTDGYWL--LEGQCLDIDEC--RY--GYCQ 178  
 |::|::| : | : |::| : | : | : | : | : | : | : | : | : | : | :  
 Db 268 TRCDVNECAPPAEPGKGHRCVNSPGSFRCCKTGYYPDGISRMCDVNECQRYPGRLCG 327  
 Qy 179 QLCANVPGYSYCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYEL 238  
 | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
 Db 328 HKCNTLGSYVCSVSGVRLSVDGRSCEDINBCSS-SPCSQECANVYGSYQCYCRRGYQL 386  
 Qy 239 EE-DGVHCSMDMECSF--SEFLCQHECVNQPGTGYFCSCP-PGYILLDDNRSCQDINECEH 294  
 : | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
 Db 387 SDVDGVTCEIDICALPTGGHICSYRCINIPGSFQCSFASGLRLAPNGRNQCQDIDECVT 446  
 Qy 295 RNHTCNLQQTTCYNLQGGFKCIDPIRCEPYLRISDNRC-MCPA-ENPGCRDQPFITILYRD 352  
 | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
 Db 447 GIHNCINBTCPNIGGFRCL-AFECPENYRRSAATRCERLPCHENRECSKPLRITYH 505  
 Qy 353 MDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKG 412  
 : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :



QY 130 ECATDSHCNPTQICINTEGGYTCSCTDGYW--LLEGQCLDIDECRY--GYCQQLCANV 184  
 Db 360 ECSSSDQPCGEGHVINCIPGNRYRCECKSGYSFVLSRTCIDINECRYPGRILCAHKCENT 419  
 QY 185 PGSYCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGV 243  
 Db 420 PGSYCTCTMTGFKLSSDGRSCEDLNECES-SPCSQECANVYGSYQCYCRRGQLSDIDGI 478  
 QY 244 HCSMDMECSF--SEPLCQHECVNQPPTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCN 300  
 Db 479 SCEDIDECALPTGGHICSFRCINIPGSFQCTCPSTGYRLAPNARNQQDIDECVAETHNCS 538  
 QY 301 LQQTCTYNLQGGFKCIDPIRCEEPYLRISDN-----RCM--CPAENPGC-RDQPTTI 348  
 Db 539 FNETCFNIQGGPRCLS-LECPENYRKSGDTRVRLEKTDITIRCIKSCRFNDVNCVLDPVHTI 597  
 QY 349 LYRDMDVVSGRSV--PADIFQMQA-TTRYPG--AYYIFQIKSGNEGREF----YMRQTG 398  
 Db 598 SHTVILSLPTFREFTREPIEIIPLRAITPTYPANQADIIFDITEGNLRESFDIIKRYM--DG 655  
 QY 399 PISATLWMTPIKGPRIQLDLEM-ITVMTVINFRGSSVIRLRIYVSQYFF 448  
 Db 656 MTGVGVVRQVRPIVGPFAILKLENNYVMGGVVSHR--NIVNVHIFVSEYWF 704

# RESULT 12

Q9Y3V7

ID Q9Y3V7 PRELIMINARY; PRT; 576 AA.  
 AC Q9Y3V7;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN DKFZP586A1519.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OK NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL050095; CAB43267.1; -.  
 DR HSSP; P00736; IAPQ.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR Pfam; PF00008; EGF; 6.  
 DR SMART; SM00179; EGF\_CA; 8.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 4.  
 DR PROSITE; PS01186; EGF\_2; 4.  
 DR PROSITE; PS01187; EGF\_CA; 9.  
 KW Hypothetical protein; EGF-like domain.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 576 AA; 63274 MW; FF2F0E9B185D8AC3 CRC64;





RL (In) Unknown A. (eds.);  
 RL ABSTRACTS OF THE 52ND ANNUAL MEETING OF THE AMERICAN SOCIETY OF HUMAN  
 RL GENETICS, pp.323-323, Unknown Publisher (2002).  
 DR EMBL; AY130458; AAN05435.1; -.  
 DR EMBL; AY130456; AAN05435.1; JOINED.  
 DR EMBL; AY130457; AAN05435.1; JOINED.  
 SQ SEQUENCE 1231 AA; 131853 MW; 0A75D1C27F258D48 CRC64;

Query Match 28.0%; Score 710.5; DB 4; Length 1231;  
 Best Local Similarity 34.3%; Pred. No. 1.2e-60;  
 Matches 146; Conservative 61; Mismatches 156; Indels 63; Gaps 12;

```

Qy      15 LCLPSPGN---AQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIP 70
      || : |: | : : || | | :|:|:| :| :| | | :| :| | |
Db      827 LCQNTKGSFYCQARQR CMDGF-LQDPEGNCVDINECTSLSEPCRFPGFSCINTVGSYTC-- 883

Qy      71 RTNPVYRGPSYNPYSTPYSGPYFAAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVD 129
      ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      884 -----QRNPLICARGYHASDDGXKCV DVN 907

Qy      130 ECATDSHQCNPTQICINTEGGYTCSDTGYW--LLEGQCLDIDECRYG--YCQQLCANV 184
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      908 ECETGVHRCGEGQVCHNLPGSYRCCKAGFQRDAFGRGCDIVNECWASPGRLCQHTCENT 967

Qy      185 PGYSYCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNNTYGSFICRCDPGYELEEDGVH 244
      ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      968 LGSYRCSCASGFLAADGKRCEQDVNECEAQR-CSQECANIYGSYQCYCRQGYQLAEDGHT 1026

Qy      245 CSDMDECS-FSEFLQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECHRNHTCNLQ 302
      |:|:|:| : | | | | | | | | | | | | | | | | | | | | |
Db      1027 CTDIDECAGAGILCTFRCLNVFGSYQCACPEQGYTMTANGRSCKDDVBCALGTHNCSEA 1086

Qy      303 QTCYNLQGGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVV 356
      :|:|:|:| | | | | | | | | | | | | | | | | | | | | |
Db      1087 ETCHNIQGSFRCL-RFECPPNYVQVSKTKC---ERTTCHDFLEQNSPARITHYQLNFG 1141

Qy      357 SGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRI 416
      :| | | | | : | | | | | | | | | | | | | | | | | | | |
Db      1142 TGLLVPAHIFRIGPAPAFPTGDTIALNIKGNBEGYFGTTRLNAYTGVVYLQRAVLEPRDF 1201

Qy      417 QLDLEM 422
      ||:| |
Db      1202 ALDVEM 1207
  
```

# RESULT 14

Q8IUI0

ID Q8IUI0 PRELIMINARY; PRT; 1231 AA.  
 AC Q8IUI0;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Fibulin 2.  
 GN FBLN2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



DE Hypothetical protein NT2RP3003649.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBT\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,  
 RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,  
 RA Nagahari K., Sugano S., Isogai T.;  
 RT "HRI human cDNA sequencing project.";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK075566; BAC11705.1; -.  
 DR InterPro; IPR000020; Anaphylatoxin.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR006210; IEGF.  
 DR Pfam; PF01821; ANATO; 1.  
 DR Pfam; PF00008; EGF; 4.  
 DR SMART; SM00181; EGF; 9.  
 DR SMART; SM00179; EGF\_CA; 9.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 4.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_CA; 8.  
 KW Hypothetical protein.  
 SQ SEQUENCE 638 AA; 70577 MW; EBC0DE3147A7621F CRC64;

Query Match 27.5%; Score 696.5; DB 4; Length 638;  
 Best Local Similarity 34.2%; Pred. No. 1.4e-59;  
 Matches 161; Conservative 66; Mismatches 151; Indels 93; Gaps 22;

```

Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDDMMCVNQNGGYLCIPRTNPV 75
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      223 CRP-----KLQCKSGFIQD-ALGNCIDINECLISAPCPIGHTCINTEGSYTC----- 269

Qy      76 YRGYPYSPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD 134
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      270 -----QKNVFN-----CGRGYHLNEEGTRCVDVDECAEP 298

Qy      135 SHQCNPTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS 189
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      299 AEPCKGKHCRCVNSPSPGFRCECKTGYYFDGISRMCDVNECQRYPGRLCGHKCENTLSYL 358

Qy      190 CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYBLEE-DGVHCSDM 248
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      359 CSCSVGFRLLSVDRSCBEDINECSS-SFCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDI 417

Qy      249 DECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQT 305
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      418 DECALPTGHHICSYRCINIPGSFQSCSPSSGYRLAPNGRNCQDIDBCVTGIHNCINETC 477

Qy      306 YNLQGGPKCIDPIRCEBPYLRISDN-----RCMCPAENPGCRDQPTTILYRDMDVV 356
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      478 FNIQGGFRCL-AFECPENYRRAATLQQEKTDTVRCI-----KSCRPNVDVTCVDPVHTI 531

Qy      357 SGRSV-----PADIFQMQA-TTRYPG--AYYIFQIKSGNEGREF-----YMRQTG 398

```

Db	532	SHTVISLPTFREFTRPBEEIIFLRAITPPHPASQANIIFDITEGNLRDSPDIKRYM--DG	589
Qy	399	PISATLVMTRPIKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF	448
Db	590	MTVGVVVRQVRPIVGPFHAVLKLEMNYVVGGVVSHR--NVVNVHIFVSEYWF	638

Search completed: January 9, 2004, 12:36:56  
 Job time : 36.4615 secs